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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: BIRKELUND, Svend
CHRISTIANSEN, Gunna
HEBSGAARD PEDERSEN, Anna-Sofie
MYGIND, Per
KNUDSEN, Katrine

(ii) TITLE OF INVENTION: SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE

(iii) NUMBER OF SEQUENCES: 30

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20001

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/446,677
(B) FILING DATE: 24-MAR-2000

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/DK98/00266
(B) FILING DATE: 19-JUN-1998

vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: DK 0744/97
(B) FILING DATE: 23-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: COOPER, Iver P.
(B) REGISTRATION NUMBER: 28,005
(C) REFERENCE/DOCKET NUMBER: BIRKELUND=1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-628-5197
(B) TELEFAX: 202-737-3528

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 205...2987

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAATGTCGAA GAGAGCACTA ACCAGGAAAA TTGCGATTTC ATAAACCCAC TTTATTATTA	60
AATTCTTACT TGCCTCATAT AAAATAGAAA ACTCAGAGAG TCAAGATAAA AATTCTTGAC	120
AGCTGTTTG TCATCTTAA CTTGATTAC TTATTTGTT TCTATATTGA TGCGAATAGT	180
TCTCTAAAAA ACAAAAGCAT TACC ATG AAG ACT TCG ATT CCT TGG GTT TTA	231
Met Lys Thr Ser Ile Pro Trp Val Leu	
1 5	
GTT TCC TCC GTG TTA GCT TTC TCA TGT CAC CTA CAG TCA CTA GCT AAC	279
Val Ser Ser Val Leu Ala Phe Ser Cys His Leu Gln Ser Leu Ala Asn	
10 15 20 25	
GAG GAA CTT TTA TCA CCT GAT GAT AGC TTT AAT GGA AAT ATC GAT TCA	327
Glu Glu Leu Leu Ser Pro Asp Asp Ser Phe Asn Gly Asn Ile Asp Ser	
30 35 40	
GGA ACG TTT ACT CCA AAA ACT TCA GCC ACA ACA TAT TCT CTA ACA GGA	375
Gly Thr Phe Thr Pro Lys Thr Ser Ala Thr Thr Tyr Ser Leu Thr Gly	
45 50 55	
GAT GTC TTC TTT TAC GAG CCT GGA AAA GGC ACT CCC TTA TCT GAC AGT	423
Asp Val Phe Phe Tyr Glu Pro Gly Lys Gly Thr Pro Leu Ser Asp Ser	
60 65 70	
TGT TTT AAG CAA ACC ACG GAC AAT CTT ACC TTC TTG GGG AAC GGT CAT	471
Cys Phe Lys Gln Thr Thr Asp Asn Leu Thr Phe Leu Gly Asn Gly His	
75 80 85	
AGC TTA ACG TTT GGC TTT ATA GAT GCT GGC ACT CAT GCA GGT GCT GCT	519
Ser Leu Thr Phe Gly Ile Asp Ala Gly Thr His Ala Gly Ala Ala	
90 95 100 105	
GCA TCT ACA ACA GCA AAT AAG AAT CTT ACC TTC TCA GGG TTT TCC TTA	567
Ala Ser Thr Thr Ala Asn Lys Asn Leu Thr Phe Ser Gly Phe Ser Leu	
110 115 120	
CTG AGT TTT GAT TCC TCT CCT AGC ACA ACG GTT ACT ACA GGT CAG GGA	615
Leu Ser Phe Asp Ser Ser Pro Ser Thr Thr Val Thr Thr Gly Gln Gly	
125 130 135	
ACG CTT TCC TCA GCA GGA GGC GTA AAT TTA GAA AAT ATT CGT AAA CTT	663
Thr Leu Ser Ser Ala Gly Gly Val Asn Leu Glu Asn Ile Arg Lys Leu	
140 145 150	
GTA GTT GCT GGG AAT TTT TCT ACT GCA GAT GGT GGA GCT ATC AAA GGA	711
Val Val Ala Gly Asn Phe Ser Thr Ala Asp Gly Gly Ala Ile Lys Gly	
155 160 165	
GCG TCT TTC CTT TTA ACT GGC ACT TCT GGA GAT GCT CTT TTT AGT AAC	759
Ala Ser Phe Leu Leu Thr Gly Thr Ser Gly Asp Ala Leu Phe Ser Asn	

170	175	180	185	
AAC TCT TCA TCA ACA AAG GGA GGA GCA ATT GCT ACT ACA GCA GGC GCT Asn Ser Ser Ser Thr Lys Gly Gly Ala Ile Ala Thr Thr Ala Gly Ala 190	195	200		807
CGC ATA GCA AAT AAC ACA GGT TAT GTT AGA TTC CTA TCT AAC ATA GCG Arg Ile Ala Asn Asn Thr Gly Tyr Val Arg Phe Leu Ser Asn Ile Ala 205	210	215		855
TCT ACG TCA GGA GGC GCT ATC GAT GAT GAA GGC ACG TCG ATA CTA TCG Ser Thr Ser Gly Gly Ala Ile Asp Asp Glu Gly Thr Ser Ile Leu Ser 220	225	230		903
AAC AAC AAA TTT CTA TAT TTT GAA GGG AAT GCA GCG AAA ACT ACT GGC Asn Asn Lys Phe Leu Tyr Phe Glu Gly Asn Ala Ala Lys Thr Thr Gly 235	240	245		951
GGT GCG ATC TGC AAC ACC AAG GCG AGT GGA TCT CCT GAA CTG ATA ATC Gly Ala Ile Cys Asn Thr Lys Ala Ser Gly Ser Pro Glu Leu Ile Ile 250	255	260	265	999
TCT AAC AAT AAG ACT CTG ATC TTT GCT TCA AAC GTA GCA GAA ACA AGC Ser Asn Asn Lys Thr Leu Ile Phe Ala Ser Asn Val Ala Glu Thr Ser 270	275	280		1047
GGT GGC GCC ATC CAT GCT AAA AAG CTA GCC CTT TCC TCT GGA GGC TTT Gly Gly Ala Ile His Ala Lys Lys Leu Ala Leu Ser Ser Gly Gly Phe 285	290	295		1095
ACA GAG TTT CTA CGA AAT AAT GTC TCA TCA GCA ACT CCT AAG GGG GGT Thr Glu Phe Leu Arg Asn Asn Val Ser Ser Ala Thr Pro Lys Gly Gly 300	305	310		1143
GCT ATC AGC ATC GAT GCC TCA GGA GAG CTC AGT CTT TCT GCA GAG ACA Ala Ile Ser Ile Asp Ala Ser Gly Glu Leu Ser Leu Ser Ala Glu Thr 315	320	325		1191
GGA AAC ATT ACC TTT GTA AGA AAT ACC CTT ACA ACA ACC GGA AGT ACC Gly Asn Ile Thr Phe Val Arg Asn Thr Leu Thr Thr Thr Gly Ser Thr 330	335	340	345	1239
GAT ACT CCT AAA CGT AAT GCG ATC AAC ATA GGA AGT AAC GGG AAA TTC Asp Thr Pro Lys Arg Asn Ala Ile Asn Ile Gly Ser Asn Gly Lys Phe 350	355	360		1287
ACG GAA TTA CGG GCT GCT AAA AAT CAT ACA ATT TTC TTC TAT GAT CCC Thr Glu Leu Arg Ala Ala Lys Asn His Thr Ile Phe Phe Tyr Asp Pro 365	370	375		1335
ATC ACT TCA GAA GGA ACC TCA TCA GAC GTA TTG AAG ATA AAT AAC GGC Ile Thr Ser Glu Gly Thr Ser Ser Asp Val Leu Lys Ile Asn Asn Gly 380	385	390		1383
TCT GCG GGA GCT CTC AAT CCA TAT CAA GGA ACG ATT CTA TTT TCT GGA Ser Ala Gly Ala Leu Asn Pro Tyr Gln Gly Thr Ile Leu Phe Ser Gly 395	400	405		1431

GAA ACC CTA ACA GCA GAT GAA CTT AAA GTT GCT GAC AAT TTA AAA TCT Glu Thr Leu Thr Ala Asp Glu Leu Lys Val Ala Asp Asn Leu Lys Ser 410 415 420 425	1479
TCA TTC ACG CAG CCA GTC TCC CTA TCC GGA GGA AAG TTA TTG CTA CAA Ser Phe Thr Gln Pro Val Ser Leu Ser Gly Gly Lys Leu Leu Gln 430 435 440	1527
AAG GGA GTC ACT TTA GAG AGC ACG AGC TTC TCT CAA GAG GCC GGT TCT Lys Gly Val Thr Leu Glu Ser Thr Ser Phe Ser Gln Glu Ala Gly Ser 445 450 455	1575
CTC CTC GGC ATG GAT TCA GGA ACG ACA TTA TCA ACT ACA GCT GGG AGT Leu Leu Gly Met Asp Ser Gly Thr Thr Leu Ser Thr Thr Ala Gly Ser 460 465 470	1623
ATT ACA ATC ACG AAC CTA GGA ATC AAT GTT GAC TCC TTA GGT CTT AAG Ile Thr Ile Thr Asn Leu Gly Ile Asn Val Asp Ser Leu Gly Leu Lys 475 480 485	1671
CAG CCC GTC AGC CTA ACA GCA AAA GGT GCT TCA AAT AAA GTG ATC GTA Gln Pro Val Ser Leu Thr Ala Lys Gly Ala Ser Asn Lys Val Ile Val 490 495 500 505	1719
TCT GGG AAG CTC AAC CTG ATT GAT ATT GAA GGG AAC ATT TAT GAA AGT Ser Gly Lys Leu Asn Leu Ile Asp Ile Glu Gly Asn Ile Tyr Glu Ser 510 515 520	1767
CAT ATG TTC AGC CAT GAC CAG CTC TTC TCT CTA TTA AAA ATC ACG GTT His Met Phe Ser His Asp Gln Leu Phe Ser Leu Leu Lys Ile Thr Val 525 530 535	1815
GAT GCT GAT GTT GAT ACT AAC GTT GAC ATC AGC AGC CTT ATC CCT GTT Asp Ala Asp Val Asp Thr Asn Val Asp Ile Ser Ser Leu Ile Pro Val 540 545 550	1863
CCT GCT GAG GAT CCT AAT TCA GAA TAC GGA TTC CAA GGA CAA TGG AAT Pro Ala Glu Asp Pro Asn Ser Glu Tyr Gly Phe Gln Gly Gln Trp Asn 555 560 565	1911
GTT AAT TGG ACT ACG GAT ACA GCT ACA AAT ACA AAA GAG GCC ACG GCA Val Asn Trp Thr Thr Asp Thr Ala Thr Asn Thr Lys Glu Ala Thr Ala 570 575 580 585	1959
ACT TGG ACC AAA ACA GGA TTT GTT CCC AGC CCC GAA AGA AAA TCT GCG Thr Trp Thr Lys Thr Gly Phe Val Pro Ser Pro Glu Arg Lys Ser Ala 590 595 600	2007
TTA GTA TGC AAT ACC CTA TGG GGA GTC TTT ACT GAC ATT CGC TCT CTG Leu Val Cys Asn Thr Leu Trp Gly Val Phe Thr Asp Ile Arg Ser Leu 605 610 615	2055
CAA CAG CTT GTA GAG ATC GGC GCA ACT GGT ATG GAA CAC AAA CAA GGT Gln Gln Leu Val Glu Ile Gly Ala Thr Gly Met Glu His Lys Gln Gly 620 625 630	2103
TTC TGG GTT TCC TCC ATG ACG AAC TTC CTG CAT AAG ACT GGA GAT GAA Phe Trp Val Ser Ser Met Thr Asn Phe Leu His Lys Thr Gly Asp Glu	2151

635	640	645	
AAT CGC AAA GGC TTC CGT CAT ACC TCT GGA GGC TAC GTC ATC GGT GGA Asn Arg Lys Gly Phe Arg His Thr Ser Gly Gly Tyr Val Ile Gly Gly 650 655 660 665			2199
AGT GCT CAC ACT CCT AAA GAC GAC CTA TTT ACC TTT GCG TTC TGC CAT Ser Ala His Thr Pro Lys Asp Asp Leu Phe Thr Phe Ala Phe Cys His 670 675 680			2247
CTC TTT GCT AGA GAC AAA GAT TGT TTT ATC GCT CAC AAC AAC TCT AGA Leu Phe Ala Arg Asp Lys Asp Cys Phe Ile Ala His Asn Asn Ser Arg 685 690 695			2295
ACC TAC GGT GGA ACT TTA TTC TTC AAG CAC TCT CAT ACC CTA CAA CCC Thr Tyr Gly Thr Leu Phe Phe Lys His Ser His Thr Leu Gln Pro 700 705 710			2343
CAA AAC TAT TTG AGA TTA GGA AGA GCA AAG TTT TCT GAA TCA GCT ATA Gln Asn Tyr Leu Arg Leu Gly Arg Ala Lys Phe Ser Glu Ser Ala Ile 715 720 725			2391
GAA AAA TTC CCT AGG GAA ATT CCC CTA GCC TTG GAT GTC CAA GTT TCG Glu Lys Phe Pro Arg Glu Ile Pro Leu Ala Leu Asp Val Gln Val Ser 730 735 740 745			2439
TTC AGC CAT TCA GAC AAC CGT ATG GAA ACG CAC TAT ACC TCA TTG CCA Phe Ser His Ser Asp Asn Arg Met Glu Thr His Tyr Thr Ser Leu Pro 750 755 760			2487
GAA TCC GAA GGT TCT TGG AGC AAC GAG TGT ATA GCT GGT GGT ATC GGC Glu Ser Glu Gly Ser Trp Ser Asn Glu Cys Ile Ala Gly Gly Ile Gly 765 770 775			2535
CTA GAC CTT CCT TTT GTT CTT TCC AAC CCA CAT CCT CTT TTC AAG ACC Leu Asp Leu Pro Phe Val Leu Ser Asn Pro His Pro Leu Phe Lys Thr 780 785 790			2583
TTC ATT CCA CAG ATG AAA GTC GAA ATG GTT TAT GTA TCA CAA AAT AGC Phe Ile Pro Gln Met Lys Val Glu Met Val Tyr Val Ser Gln Asn Ser 795 800 805			2631
TTC TTC GAA AGC TCT AGT GAT GGC CGT GGT TTT AGT ATT GGA AGG CTG Phe Phe Glu Ser Ser Asp Gly Arg Gly Phe Ser Ile Gly Arg Leu 810 815 820 825			2679
CTT AAC CTC TCG ATT CCT GTG GGT GCG AAA TTC GTG CAG GGG GAT ATC Leu Asn Leu Ser Ile Pro Val Gly Ala Lys Phe Val Gln Gly Asp Ile 830 835 840			2727
GGA GAT TCC TAC ACC TAT GAT CTC TCA GGA TTC TTT GTT TCC GAT GTC Gly Asp Ser Tyr Thr Tyr Asp Leu Ser Gly Phe Phe Val Ser Asp Val 845 850 855			2775
TAT CGT AAC AAT CCC CAA TCT ACA GCG ACT CTT GTG ATG AGC CCA GAC Tyr Arg Asn Asn Pro Gln Ser Thr Ala Thr Leu Val Met Ser Pro Asp 860 865 870			2823

TCT TGG AAA ATT CGC GGT GGC AAT CTT TCA AGA CAG GCA TTT TTA CTG Ser Trp Lys Ile Arg Gly Gly Asn Leu Ser Arg Gln Ala Phe Leu Leu 875 880 885	2871
AGG GGT AGC AAC AAC TAC GTC TAC AAC TCC AAT TGT GAG CTC TTC GGA Arg Gly Ser Asn Asn Tyr Val Tyr Asn Ser Asn Cys Glu Leu Phe Gly 890 895 900 905	2919
CAT TAC GCT ATG GAA CTC CGT GGA TCT TCA AGG AAC TAC AAT GTA GAT His Tyr Ala Met Glu Leu Arg Gly Ser Ser Arg Asn Tyr Asn Val Asp 910 915 920	2967
GTT GGT ACC AAA CTC CGA TT CTAGATTGCT AAAACTCCCT AGTTCTTCTA GGGAG Val Gly Thr Lys Leu Arg Phe 925	3022
TTTTCTCATA CTTTAGGGA AATATTGCT ATAGGGAATG CTTTCCTTGC AAACTGTAAA AAATAACATT TGCCCTCTT CAAAAAAGAT TTCTTTAAT AATTCTAGT TATAATTAA TTTAAAAAAC AGTTAAATAA TTAATAGACA ATAATCTATT CTTATTGACT TCTTTTTT	3082 3142 3200

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 928 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Thr Ser Ile Pro Trp Val Leu Val Ser Ser Val Leu Ala Phe 1 5 10 15
Ser Cys His Leu Gln Ser Leu Ala Asn Glu Glu Leu Leu Ser Pro Asp 20 25 30
Asp Ser Phe Asn Gly Asn Ile Asp Ser Gly Thr Phe Thr Pro Lys Thr 35 40 45
Ser Ala Thr Thr Tyr Ser Leu Thr Gly Asp Val Phe Phe Tyr Glu Pro 50 55 60
Gly Lys Gly Thr Pro Leu Ser Asp Ser Cys Phe Lys Gln Thr Thr Asp 65 70 75 80
Asn Leu Thr Phe Leu Gly Asn Gly His Ser Leu Thr Phe Gly Phe Ile 85 90 95
Asp Ala Gly Thr His Ala Gly Ala Ala Ser Thr Thr Ala Asn Lys 100 105 110
Asn Leu Thr Phe Ser Gly Phe Ser Leu Leu Ser Phe Asp Ser Ser Pro 115 120 125
Ser Thr Thr Val Thr Thr Gly Gln Gly Thr Leu Ser Ser Ala Gly Gly

130	135	140
Val Asn Leu Glu Asn Ile Arg Lys Leu Val Val Ala Gly Asn Phe Ser		
145	150	155
160		
Thr Ala Asp Gly Gly Ala Ile Lys Gly Ala Ser Phe Leu Leu Thr Gly		
165	170	175
Thr Ser Gly Asp Ala Leu Phe Ser Asn Asn Ser Ser Ser Thr Lys Gly		
180	185	190
Gly Ala Ile Ala Thr Thr Ala Gly Ala Arg Ile Ala Asn Asn Thr Gly		
195	200	205
Tyr Val Arg Phe Leu Ser Asn Ile Ala Ser Thr Ser Gly Gly Ala Ile		
210	215	220
Asp Asp Glu Gly Thr Ser Ile Leu Ser Asn Asn Lys Phe Leu Tyr Phe		
225	230	235
240		
Glu Gly Asn Ala Ala Lys Thr Thr Gly Gly Ala Ile Cys Asn Thr Lys		
245	250	255
Ala Ser Gly Ser Pro Glu Leu Ile Ile Ser Asn Asn Lys Thr Leu Ile		
260	265	270
Phe Ala Ser Asn Val Ala Glu Thr Ser Gly Gly Ala Ile His Ala Lys		
275	280	285
Lys Leu Ala Leu Ser Ser Gly Gly Phe Thr Glu Phe Leu Arg Asn Asn		
290	295	300
Val Ser Ser Ala Thr Pro Lys Gly Gly Ala Ile Ser Ile Asp Ala Ser		
305	310	315
320		
Gly Glu Leu Ser Leu Ser Ala Glu Thr Gly Asn Ile Thr Phe Val Arg		
325	330	335
Asn Thr Leu Thr Thr Gly Ser Thr Asp Thr Pro Lys Arg Asn Ala		
340	345	350
Ile Asn Ile Gly Ser Asn Gly Lys Phe Thr Glu Leu Arg Ala Ala Lys		
355	360	365
Asn His Thr Ile Phe Phe Tyr Asp Pro Ile Thr Ser Glu Gly Thr Ser		
370	375	380
385		
Ser Asp Val Leu Lys Ile Asn Asn Gly Ser Ala Gly Ala Leu Asn Pro		
390	395	400
Tyr Gln Gly Thr Ile Leu Phe Ser Gly Glu Thr Leu Thr Ala Asp Glu		
405	410	415
Leu Lys Val Ala Asp Asn Leu Lys Ser Ser Phe Thr Gln Pro Val Ser		
420	425	430
Leu Ser Gly Gly Lys Leu Leu Leu Gln Lys Gly Val Thr Leu Glu Ser		
435	440	445

Thr Ser Phe Ser Gln Glu Ala Gly Ser Leu Leu Gly Met Asp Ser Gly
 450 455 460

Thr Thr Leu Ser Thr Thr Ala Gly Ser Ile Thr Ile Thr Asn Leu Gly
 465 470 475 480

Ile Asn Val Asp Ser Leu Gly Leu Lys Gln Pro Val Ser Leu Thr Ala
 485 490 495

Lys Gly Ala Ser Asn Lys Val Ile Val Ser Gly Lys Leu Asn Leu Ile
 500 505 510

Asp Ile Glu Gly Asn Ile Tyr Glu Ser His Met Phe Ser His Asp Gln
 515 520 525

Leu Phe Ser Leu Leu Lys Ile Thr Val Asp Ala Asp Val Asp Thr Asn
 530 535 540

Val Asp Ile Ser Ser Leu Ile Pro Val Pro Ala Glu Asp Pro Asn Ser
 545 550 555 560

Glu Tyr Gly Phe Gln Gly Gln Trp Asn Val Asn Trp Thr Thr Asp Thr
 565 570 575

Ala Thr Asn Thr Lys Glu Ala Thr Ala Thr Trp Thr Lys Thr Gly Phe
 580 585 590

Val Pro Ser Pro Glu Arg Lys Ser Ala Leu Val Cys Asn Thr Leu Trp
 595 600 605

Gly Val Phe Thr Asp Ile Arg Ser Leu Gln Gln Leu Val Glu Ile Gly
 610 615 620

Ala Thr Gly Met Glu His Lys Gln Gly Phe Trp Val Ser Ser Met Thr
 625 630 635 640

Asn Phe Leu His Lys Thr Gly Asp Glu Asn Arg Lys Gly Phe Arg His
 645 650 655

Thr Ser Gly Gly Tyr Val Ile Gly Gly Ser Ala His Thr Pro Lys Asp
 660 665 670

Asp Leu Phe Thr Phe Ala Phe Cys His Leu Phe Ala Arg Asp Lys Asp
 675 680 685

Cys Phe Ile Ala His Asn Asn Ser Arg Thr Tyr Gly Gly Thr Leu Phe
 690 695 700

Phe Lys His Ser His Thr Leu Gln Pro Gln Asn Tyr Leu Arg Leu Gly
 705 710 715 720

Arg Ala Lys Phe Ser Glu Ser Ala Ile Glu Lys Phe Pro Arg Glu Ile
 725 730 735

Pro Leu Ala Leu Asp Val Gln Val Ser Phe Ser His Ser Asp Asn Arg
 740 745 750

Met Glu Thr His Tyr Thr Ser Leu Pro Glu Ser Gly Ser Trp Ser
 755 760 765

Asn Glu Cys Ile Ala Gly Gly Ile Gly Leu Asp Leu Pro Phe Val Leu
 770 775 780

Ser Asn Pro His Pro Leu Phe Lys Thr Phe Ile Pro Gln Met Lys Val
 785 790 795 800

Glu Met Val Tyr Val Ser Gln Asn Ser Phe Phe Glu Ser Ser Asp
 805 810 815

Gly Arg Gly Phe Ser Ile Gly Arg Leu Leu Asn Leu Ser Ile Pro Val
 820 825 830

Gly Ala Lys Phe Val Gln Gly Asp Ile Gly Asp Ser Tyr Thr Tyr Asp
 835 840 845

Leu Ser Gly Phe Phe Val Ser Asp Val Tyr Arg Asn Asn Pro Gln Ser
 850 855 860

Thr Ala Thr Leu Val Met Ser Pro Asp Ser Trp Lys Ile Arg Gly Gly
 865 870 875 880

Asn Leu Ser Arg Gln Ala Phe Leu Leu Arg Gly Ser Asn Asn Tyr Val
 885 890 895

Tyr Asn Ser Asn Cys Glu Leu Phe Gly His Tyr Ala Met Glu Leu Arg
 900 905 910

Gly Ser Ser Arg Asn Tyr Asn Val Asp Val Gly Thr Lys Leu Arg Phe
 915 920 925

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2815 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAAATCGC	AATTTCTTG	GTTAGTGCTC	TCTTCGACAT	TGGCATGTTT	TACTAGTTGT	60
TCCACTGTTT	TTGCTGCAAC	TGCTGAAAAT	ATAGGCCCCT	CTGATAGCTT	TGACGGAAGT	120
ACTAACACAG	GCACCTATAAC	TCCTAAAAAT	ACGACTACTG	GAATAGACTA	TACTCTGACA	180
GGAGATATAA	CTCTGCCAAA	CCTTGGGGAT	TCGGCAGCTT	TAACGAAGGG	TTGTTTTCT	240
GACACTACGG	AATCTTTAAG	CTTGCCGGT	AAGGGGTACT	CACTTTCTTT	TTAAATATT	300
AAGTCTAGTG	CTGAAGGCGC	AGCACTTTCT	GTTACAAC TG	ATAAAAATCT	GTCGCTAAC	360
GGATTTTCGA	GTCTTACTTT	CTTAGCGGCC	CCATCATCGG	TAATCACAAAC	CCCCTCAGGA	420
AAAGGTGCAG	TTAAATGTGG	AGGGGATCTT	ACATTTGATA	ACAATGGAAC	TATTTTATT	480
AAACAAGATT	ACTGTGAGGA	AAATGGCGGA	GCCATTCTCA	CCAAGAATCT	TTCTTGAAA	540
AACAGCACGG	GATCGATTTC	TTTGAAAGGG	AATAATCGA	GCGAACAGG	GAAAAAAGGT	600
GGGGCTATTT	GTGCTACTGG	TACTGTAGAT	ATTACAAATA	ATACGGCTCC	TACCCTCTTC	660
TCGAACAATA	TTGCTGAAGC	TGCAGGTGGA	GCTATAAATA	GCACAGGAAA	CTGTACAATT	720
ACAGGGAATA	CGTCTTGT	ATTTTCTGAA	AATAGTGTGA	CAGCGACCGC	AGGAAATGGA	780

GGAGCTCTTT	CTGGAGATGC	CGATGTTACC	ATATCTGGGA	ATCAGAGTGT	AACTTTCTCA	840
GGAAACCAAG	CTGTAGCTAA	TGGCGGAGCC	ATTATGCTA	AGAAGCTTAC	ACTGGCTTC	900
GGGGGGGGGG	GGGGTATCTC	CTTTTCTAAC	AATATACTGC	AAGGTACCAAC	TGCAGGTAAT	960
GGTGGAGCCA	TTTCTATACT	GGCAGCTGGA	GAGTGTAGTC	TTTCAGCAGA	AGCAGGGGAC	1020
ATTACCTTCA	ATGGGAATGC	CATTGTTGCA	ACTACACCAC	AAACTACAAA	AAGAAATTCT	1080
ATTGACATAG	GATCTACTGC	AAAGATCACG	AATTACGTG	CAATATCTGG	GCATAGCATC	1140
TTTTCTACG	ATCCGATTAC	TGCTAATACG	GCTGCGGATT	CTACAGATAC	TTAAATCTC	1200
AATAAGGCTG	ATGCAGGTAA	TAGTACAGAT	TATAGTGGGT	CGATTGTTT	TTCTGGTGA	1260
AAGCTCTCTG	AAGATGAAGC	AAAAGTTGCA	GACAACCTCA	CTTCTACGCT	GAAGCAGCCT	1320
GTAACACTAA	CTGCAGGAAA	TTTAGTACTT	AAACGTGGTG	TCACTCTCGA	TACGAAAGGC	1380
TTTACTCAGA	CCGCGGGTTC	CTCTGTTATT	ATGGATGCGG	GCACAAACGTT	AAAAGCAAGT	1440
ACAGAGGAGG	TCACCTTAAC	AGGTCTTCC	ATTCTGTAG	ACTCTTTAGG	CGAGGGTAAG	1500
AAAGTTGTAA	TTGCTGCTTC	TGCAGCAAGT	AAAAATGTAG	CCCTTAGTGG	TCCGATTCTT	1560
CTTTGGATA	ACCAAGGGAA	TGCTTATGAA	AATCACGACT	TAGGAAAAAC	TCAAGACTTT	1620
TCATTGTGC	AGCTCTCTGC	TCTGGTACT	GCAACAACTA	CAGATGTTCC	AGCGGTTCC	1680
ACAGTAGCAA	CTCCTACGCA	CTATGGGTAT	CAAGGTACTT	GGGAAATGAC	TTGGGTTGAT	1740
GATACCGCAA	GCACCTCCAAA	GACTAAGACA	GCGACATTAG	CTTGGACCAA	TACAGGCTAC	1800
CTTCCGAATC	CTGAGCGTCA	AGGACCTTTA	GTTCTTAATA	GCCTTTGGGG	ATCTTTTCA	1860
GACATCCAAG	CGATTCAAGG	TGTCATAGAG	AGAAGTGCTT	TGACTCTTTG	TTAGATCGA	1920
GGCTTCTGGG	CTGCGGGAGT	CGCCAATTTC	TTAGATAAAAG	ATAAGAAAGG	GGAAAAACGC	1980
AAATACCGTC	ATAAAATCTGG	TGGATATGCT	ATCGGAGGTG	CAGCGCAAAC	TTGTTCTGAA	2040
AACTTAATTA	GCTTTGCCTT	TTGCCAACCT	TTGGTAGCG	ATAAAGATT	CTTAGTCGCT	2100
AAAAATCATA	CTGATACCTA	TGCAGGAGCC	TTCTATATCC	AACACATTAC	AGAATGTAGT	2160
GGGTTCATAG	GTTGTCTCTT	AGATAAAACTT	CCTGGCTCTT	GGAGTCATAA	ACCCCTCGTT	2220
TTAGAAGGGC	AGCTCGCTTA	TAGCCACGTC	AGTAATGATC	TGAAGACAAA	GTATACTGCG	2280
TATCCTGAGG	TGAAAGGTTC	TTGGGGGAAT	AATGCTTTA	ACATGATGTT	GGGAGCTTCT	2340
TCTCATTCTT	ATCCTGAATA	CCTGCATTGT	TTTGATACCT	ATGCTCCATA	CATCAAAC	2400
AATCTGACCT	ATATACTGCA	GGACAGCTTC	TCGGAGAAAG	GTACAGAAGG	AAGATCTTT	2460
GATGACAGCA	ACCTCTCAA	TTTATCTTTG	CCTATAGGGG	TGAAGTTGA	GAAGTTCTCT	2520
GATTGTAATG	ACTTTCTTA	TGATCTGACT	TTATCCTATG	TTCTGATCT	TATCCGCAAT	2580
GATCCCCAAT	GCACACTACAGC	ACTTGTAAATC	AGCGGAGCCT	CTTGGGAAAC	TTATGCCAAT	2640
AACTTAGCAC	GACAGGCCTT	GCAAGTGCCT	GCAGGGCAGTC	ACTACGCCCT	CTCTCCTATG	2700
TTTGAAGTGC	TCGGCCAGTT	TGTCTTGAA	GTTCGTGGAT	CCTCACGGAT	TTATAATGTA	2760
GATCTTGGGG	GTAAGTTCCA	ATTCTAGGAG	CGTCTCTCAT	GTCTCAGAAA	TTCTG	2815

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 928 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Lys	Ser	Gln	Phe	Ser	Trp	Leu	Val	Leu	Ser	Ser	Thr	Leu	Ala	Cys
1				5					10					15	

Phe	Thr	Ser	Cys	Ser	Thr	Val	Phe	Ala	Ala	Thr	Ala	Glu	Asn	Ile	Gly
						20			25				30		

Pro	Ser	Asp	Ser	Phe	Asp	Gly	Ser	Thr	Asn	Thr	Gly	Thr	Tyr	Thr	Pro
				35				40				45			

Lys	Asn	Thr	Thr	Thr	Gly	Ile	Asp	Tyr	Thr	Leu	Thr	Gly	Asp	Ile	Thr
				50		55			60						

Leu Gln Asn Leu Gly Asp Ser Ala Ala Leu Thr Lys Gly Cys Phe Ser
 65 70 75 80

Asp Thr Thr Glu Ser Leu Ser Phe Ala Gly Lys Gly Tyr Ser Leu Ser
 85 90 95

Phe Leu Asn Ile Lys Ser Ser Ala Glu Gly Ala Ala Leu Ser Val Thr
 100 105 110

Thr Asp Lys Asn Leu Ser Leu Thr Gly Phe Ser Ser Leu Thr Phe Leu
 115 120 125

Ala Ala Pro Ser Ser Val Ile Thr Thr Pro Ser Gly Lys Gly Ala Val
 130 135 140

Lys Cys Gly Gly Asp Leu Thr Phe Asp Asn Asn Gly Thr Ile Leu Phe
 145 150 155 160

Lys Gln Asp Tyr Cys Glu Glu Asn Gly Ala Ile Ser Thr Lys Asn
 165 170 175

Leu Ser Leu Lys Asn Ser Thr Gly Ser Ile Ser Phe Glu Gly Asn Lys
 180 185 190

Ser Ser Ala Thr Gly Lys Gly Ala Ile Cys Ala Thr Gly Thr
 195 200 205

Val Asp Ile Thr Asn Asn Thr Ala Pro Thr Leu Phe Ser Asn Asn Ile
 210 215 220

Ala Glu Ala Ala Gly Gly Ala Ile Asn Ser Thr Gly Asn Cys Thr Ile
 225 230 235 240

Thr Gly Asn Thr Ser Leu Val Phe Ser Glu Asn Ser Val Thr Ala Thr
 245 250 255

Ala Gly Asn Gly Gly Ala Leu Ser Gly Asp Ala Asp Val Thr Ile Ser
 260 265 270

Gly Asn Gln Ser Val Thr Phe Ser Gly Asn Gln Ala Val Ala Asn Gly
 275 280 285

Gly Ala Ile Tyr Ala Lys Lys Leu Thr Leu Ala Ser Gly Gly Gly
 290 295 300

Gly Ile Ser Phe Ser Asn Asn Ile Val Gln Gly Thr Thr Ala Gly Asn
 305 310 315 320

Gly Gly Ala Ile Ser Ile Leu Ala Ala Gly Glu Cys Ser Leu Ser Ala
 325 330 335

Glu Ala Gly Asp Ile Thr Phe Asn Gly Asn Ala Ile Val Ala Thr Thr
 340 345 350

Pro Gln Thr Thr Lys Arg Asn Ser Ile Asp Ile Gly Ser Thr Ala Lys
 355 360 365

Ile Thr Asn Leu Arg Ala Ile Ser Gly His Ser Ile Phe Phe Tyr Asp
 370 375 380

Pro Ile Thr Ala Asn Thr Ala Ala Asp Ser Thr Asp Thr Leu Asn Leu
 385 390 395 400

Asn Lys Ala Asp Ala Gly Asn Ser Thr Asp Tyr Ser Gly Ser Ile Val
 405 410 415

Phe Ser Gly Glu Lys Leu Ser Glu Asp Glu Ala Lys Val Ala Asp Asn
 420 425 430

Leu Thr Ser Thr Leu Lys Gln Pro Val Thr Leu Thr Ala Gly Asn Leu
 435 440 445

Val Leu Lys Arg Gly Val Thr Leu Asp Thr Lys Gly Phe Thr Gln Thr
 450 455 460

Ala Gly Ser Ser Val Ile Met Asp Ala Gly Thr Thr Leu Lys Ala Ser
 465 470 475 480

Thr Glu Glu Val Thr Leu Thr Gly Leu Ser Ile Pro Val Asp Ser Leu
 485 490 495

Gly Glu Gly Lys Lys Val Val Ile Ala Ala Ser Ala Ala Ser Lys Asn
 500 505 510

Val Ala Leu Ser Gly Pro Ile Leu Leu Leu Asp Asn Gln Gly Asn Ala
 515 520 525

Tyr Glu Asn His Asp Leu Gly Lys Thr Gln Asp Phe Ser Phe Val Gln
 530 535 540

Leu Ser Ala Leu Gly Thr Ala Thr Thr Asp Val Pro Ala Val Pro
 545 550 555 560

Thr Val Ala Thr Pro Thr His Tyr Gly Tyr Gln Gly Thr Trp Gly Met
 565 570 575

Thr Trp Val Asp Asp Thr Ala Ser Thr Pro Lys Thr Lys Thr Ala Thr
 580 585 590

Leu Ala Trp Thr Asn Thr Gly Tyr Leu Pro Asn Pro Glu Arg Gln Gly
 595 600 605

Pro Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Ser Asp Ile Gln Ala
 610 615 620

Ile Gln Gly Val Ile Glu Arg Ser Ala Leu Thr Leu Cys Ser Asp Arg
 625 630 635 640

Gly Phe Trp Ala Ala Gly Val Ala Asn Phe Leu Asp Lys Asp Lys Lys
 645 650 655

Gly Glu Lys Arg Lys Tyr Arg His Lys Ser Gly Gly Tyr Ala Ile Gly
 660 665 670

Gly Ala Ala Gln Thr Cys Ser Glu Asn Leu Ile Ser Phe Ala Phe Cys

675	680	685
Gln Leu Phe Gly Ser Asp Lys Asp Phe Leu Val Ala Lys Asn His Thr		
690	695	700
Asp Thr Tyr Ala Gly Ala Phe Tyr Ile Gln His Ile Thr Glu Cys Ser		
705	710	715
720		
Gly Phe Ile Gly Cys Leu Leu Asp Lys Leu Pro Gly Ser Trp Ser His		
725	730	735
Lys Pro Leu Val Leu Glu Gly Gln Leu Ala Tyr Ser His Val Ser Asn		
740	745	750
Asp Leu Lys Thr Lys Tyr Thr Ala Tyr Pro Glu Val Lys Gly Ser Trp		
755	760	765
Gly Asn Asn Ala Phe Asn Met Met Leu Gly Ala Ser Ser His Ser Tyr		
770	775	780
Pro Glu Tyr Leu His Cys Phe Asp Thr Tyr Ala Pro Tyr Ile Lys Leu		
785	790	795
800		
Asn Leu Thr Tyr Ile Arg Gln Asp Ser Phe Ser Glu Lys Gly Thr Glu		
805	810	815
Gly Arg Ser Phe Asp Asp Ser Asn Leu Phe Asn Leu Ser Leu Pro Ile		
820	825	830
Gly Val Lys Phe Glu Lys Phe Ser Asp Cys Asn Asp Phe Ser Tyr Asp		
835	840	845
Leu Thr Leu Ser Tyr Val Pro Asp Leu Ile Arg Asn Asp Pro Lys Cys		
850	855	860
Thr Thr Ala Leu Val Ile Ser Gly Ala Ser Trp Glu Thr Tyr Ala Asn		
865	870	875
880		
Asn Leu Ala Arg Gln Ala Leu Gln Val Arg Ala Gly Ser His Tyr Ala		
885	890	895
Phe Ser Pro Met Phe Glu Val Leu Gly Gln Phe Val Phe Glu Val Arg		
900	905	910
Gly Ser Ser Arg Ile Tyr Asn Val Asp Leu Gly Gly Lys Phe Gln Phe		
915	920	925

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3052 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGCGATTTT	CGCTCTGCGG	ATTCCTCTA	GTTTTTCTT	TAACATTGCT	CTCAGTCTTC	60
GACACTTCTT	TGAGTGCTAC	TACGATTCT	TTAACCCAG	AAGATAAGTT	TCATGGAGAT	120
AGTCAGAATG	CAGAACGTT	TTATAATGTT	CAAGCTGGGG	ATGTCTATAG	CCTTACTGGT	180
GATGTCTCAA	TATCTAACGT	CGATAACTCT	GCATTAATA	AAGCCTGCTT	CAATGTGACC	240
TCAGGAAGTG	TGACGTTCGC	AGGAAATCAT	CATGGGTTAT	ATTTTAATAA	TATTCCTCA	300
GGAACATACAA	AGGAAGGGGC	TGTACTTTGT	TGCCAAGATC	CTCAAGAAC	GGCACGTTTT	360
TCTGGGTTCT	CCACGCTCTC	TTTTATTCA	AGCCCCGGAG	ATATTAAAGA	ACAGGGATGT	420
CTCTATTCAA	AAAATGCACT	TATGCTCTTA	AACAATTATG	TAGTGCCTT	TGAACAAAC	480
CAAAGTAAGA	CTAAAGGCAGG	AGCTATTAGT	GGGGCGAATG	TTACTATAGT	AGGCAACTAC	540
GATTCCGTC	CTTTCTATCA	GAATGCAGCC	ACTTTGGAG	GTGCTATCCA	TTCTTCAGGT	600
CCCCTACAGA	TTGCAGTAAA	TCAGGCAGAG	ATAAGATTG	CACAAAATAC	TGCCAAGAAT	660
GGTTCTGGAG	GGGCTTGTA	CTCCGATGGT	GATATTGATA	TTGATCAGAA	TGCTTATGTT	720
CTATTCGAG	AAAATGAGGC	ATTGACTACT	GCTATAGGTA	AGGGAGGGC	TGCTGTTGT	780
CTTCCCACCT	CAGGAAGTAG	TACTCCAGTT	CCTATTGTGA	CTTCTCTGA	CATAAAACAG	840
TTAGTCTTTG	AAAGAAACCA	TTCCATAATG	GGTGGCGGGAG	CCATTATGTC	TAGGAAACTT	900
AGCATCTCTT	CAGGAGGTCC	TACTCTATTT	ATCAATAATA	TATCATATGC	AAATTGCAA	960
AATTCTAGGTG	GAGCTATTGC	CATTGATACT	GGAGGGGAGA	TCAGTTTATC	AGCAGAGAAA	1020
GGAACAAATTA	CATTCCAAGG	AAACCGGAGC	AGCTTACCGT	TTTGAATGG	CATCCATCTT	1080
TTACAAAATG	CTAAATTCC	GAAATTACAG	GCGAGAAATG	GATGCTCTAT	AGAATTTTAT	1140
GATCCTATTA	CTTCTGAAGC	AGATGGGTCT	ACCCAATTGA	ATATCAACGG	AGATCCTAAA	1200
AATAAAGAGT	ACACAGGGAC	CATACTCTT	TCTGGAGAAA	AGAGTCTAGC	AAACGATCCT	1260
AGGGATTTA	AATCTACAAT	CCCTCAGAAC	GTCAACCTGT	CTGCAGGATA	CTAGTTATT	1320
AAAGAGGGGG	CCGAAGTCAC	AGTTTCAAAA	TTCACGCAGT	CTCCAGGATC	GCATTTAGTT	1380
TTAGATTTAG	GAACCAAAC	GATAGCCTCT	AAGGAAGACA	TTGCCATCAC	AGGCCTCGCG	1440
ATAGATATAG	ATAGCTTAAG	CTCATCCTCA	ACAGCAGCTG	TTATTAAAGC	AAACACCGCA	1500
AATAAACAGA	TATCCGTGAC	GGACTCTATA	GAACCTATCT	CGCCTACTGG	CAATGCCTAT	1560
GAAGATCTCA	GAATGAGAAA	TTCACAGACG	TTCCCTCTGC	TCTCTTTAGA	GCCTGGAGCC	1620
GGGGTAGTG	TGACTGTAAC	TGCTGGAGAT	TTCCCTACCGG	TAAGTCCCCA	TTATGGTTTT	1680
CAAGGCAATT	GGAAATTAGC	TTGGACAGGA	ACTGGAAACA	AAGTTGGAGA	ATTCTCTGG	1740
GATAAAATAA	ATTATAAGCC	TAGACCTGAA	AAAGAAGGAA	ATTAGTTCC	TAATATCTTG	1800
TGGGGGAATG	CTGTAAATGT	CAGATCCTTA	ATGCAGGTT	AAGAGACCCA	TGCACTGAGC	1860
TTACAGACAG	ATCGAGGGCT	GTGGATCGAT	GGAAATTGGGA	ATTCTCTCCA	TGTATCTGCC	1920
TCCGAAGACA	ATATAAGGT	CCGTCTAAC	AGCAGGTGGAT	ATGTTCTATC	TGAAATAAT	1980
GAGATCACAC	CTAACGACTA	TACTTCGATG	GCATTTCCC	AACTCTTTAG	TAGAGACAAG	2040
GACTATGCGG	TTTCCAACAA	CGAATACAGA	ATGTATTTAG	GATCGTATCT	CTATCAATAT	2100
ACAACCTCCC	TAGGGAATAT	TTTCCGTTAT	GCTTCGCGTA	ACCCCTAATGT	AAACGTCGGG	2160
ATTCTCTCAA	GAAGGTTCT	TCAAAATCCT	CTTATGATT	TTCATTTTT	GTGTGCTTAT	2220
GGTCATGCCA	CCAATGATAT	AAAAACAGAC	TACGCAAATT	TCCCTATGGT	AAAAAACAGC	2280
TGGAGAAACA	ATTGTTGGGC	TATAGAGTGC	GGAGGGAGCA	TGCCTCTATT	GGTATTTGAG	2340
AACCGGAAGAC	TTTCCAAGG	TGCCATCCCA	TTTATGAAAC	TACAATTAGT	TTATGCTTAT	2400
CAGGGAGATT	TCAAAGAGAC	GAETGCAGAT	GGCCGTAGAT	TTAGTAATGG	GAGTTAACAA	2460
TCGATTTCTG	TACCTCTAGG	CATACTGCTT	GAGAGCTGG	CACTTTCTCA	GGATGTACTC	2520
TATGACTTTA	GTTCCTCTA	TATTCTGAT	ATTTCCGTA	AGGATCCCTC	ATGTGAAGCT	2580
GCTCTGGTGA	TTAGCGGAGA	CTCCTGGCTT	GTTCCGGCAG	CACACGTATC	AAGACATGCT	2640
TTTGTAGGG	GTGGAACGGG	TCGGTATCAC	TTAACGACT	ATACTGAGCT	CTTATGTCGA	2700
GGAAGTATAG	AATGCCGCC	CCATGCTAGG	AATTATAATA	TAAACTGTGG	AAGCAAATT	2760
CGTTTTAGA	AGGTTCCAT	TGCCTGTGTG	GTTCCGGATC	TTAACTATAA	ATCCTGGACT	2820
ATGGATCATA	GGCATGGGT	TTCTCGAACT	TGTGTGGAGA	ATAACGACAT	TTTATATGCA	2880
TAACGGAATA	CTCGTATCAC	CTCAGCCCT	AGAGACATTC	TTTAGGGGTT	CTTTATTGTT	2940
CTAAACTTCG	TATTTATCG	AGAATCCTT	ACGTTCTTGG	TTTGCTTGTC	TCCGAGGAGT	3000
TCTCTAACGA	ATCATAGGGA	TTCCAGGGTT	CTGTTCCCTTG	AGTCCTTGG	A	3052

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 922 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Arg Phe Ser Leu Cys Gly Phe Pro Leu Val Phe Ser Leu Thr Leu
 1 5 10 15

Leu Ser Val Phe Asp Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr
 20 25 30

Pro Glu Asp Ser Phe His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr
 35 40 45

Asn Val Gln Ala Gly Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile
 50 55 60

Ser Asn Val Asp Asn Ser Ala Leu Asn Lys Ala Cys Phe Asn Val Thr
 65 70 75 80

Ser Gly Ser Val Thr Phe Ala Gly Asn His His Gly Leu Tyr Phe Asn
 85 90 95

Asn Ile Ser Ser Gly Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln
 100 105 110

Asp Pro Gln Ala Thr Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe
 115 120 125

Ile Gln Ser Pro Gly Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys
 130 135 140

Asn Ala Leu Met Leu Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn
 145 150 155 160

Gln Ser Lys Thr Lys Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile
 165 170 175

Val Gly Asn Tyr Asp Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe
 180 185 190

Gly Gly Ala Ile His Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln
 195 200 205

Ala Glu Ile Arg Phe Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly
 210 215 220

Ala Leu Tyr Ser Asp Gly Asp Ile Asp Ile Asp Gln Asn Ala Tyr Val
 225 230 235 240

Leu Phe Arg Glu Asn Glu Ala Leu Thr Thr Ala Ile Gly Lys Gly Gly
 245 250 255

Ala Val Cys Cys Leu Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile
 260 265 270

Val Thr Phe Ser Asp Asn Lys Gln Leu Val Phe Glu Arg Asn His Ser
 275 280 285

Ile Met Gly Gly Ala Ile Tyr Ala Arg Lys Leu Ser Ile Ser Ser
 290 295 300

Gly Gly Pro Thr Leu Phe Ile Asn Asn Ile Ser Tyr Ala Asn Ser Gln
 305 310 315 320

Asn Leu Gly Gly Ala Ile Ala Ile Asp Thr Gly Gly Glu Ile Ser Leu
 325 330 335

Ser Ala Glu Lys Gly Thr Ile Thr Phe Gln Gly Asn Arg Thr Ser Leu
 340 345 350

Pro Phe Leu Asn Gly Ile His Leu Leu Gln Asn Ala Lys Phe Leu Lys
 355 360 365

Leu Gln Ala Arg Asn Gly Cys Ser Ile Glu Phe Tyr Asp Pro Ile Thr
 370 375 380

Ser Glu Ala Asp Gly Ser Thr Gln Leu Asn Ile Asn Gly Asp Pro Lys
 385 390 395 400

Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu
 405 410 415

Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn
 420 425 430

Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val
 435 440 445

Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly
 450 455 460

Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala
 465 470 475 480

Ile Asp Ile Asp Ser Leu Ser Ser Ser Thr Ala Ala Val Ile Lys
 485 490 495

Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu
 500 505 510

Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser
 515 520 525

Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val
 530 535 540

Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe
 545 550 555 560

Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly
 565 570 575

Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu
 580 585 590

Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val Asn Val Arg
 595 600 605

Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp
 610 615 620

Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala
 625 630 635 640

Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu
 645 650 655

Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe
 660 665 670

Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu
 675 680 685

Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu
 690 695 700

Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly
 705 710 715 720

Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe
 725 730 735

Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala
 740 745 750

Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile
 755 760 765

Glu Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn Gly Arg Leu
 770 775 780

Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr
 785 790 795 800

Gln Gly Asp Phe Lys Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn
 805 810 815

Gly Ser Leu Thr Ser Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys
 820 825 830

Leu Ala Leu Ser Gln Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile
 835 840 845

Pro Asp Ile Phe Arg Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile
 850 855 860

Ser Gly Asp Ser Trp Leu Val Pro Ala Ala His Val Ser Arg His Ala
 865 870 875 880

Phe Val Gly Ser Gly Thr Gly Arg Tyr His Phe Asn Asp Tyr Thr Glu
 885 890 895

Leu Leu Cys Arg Gly Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr
 900 905 910

Asn Ile Asn Cys Gly Ser Lys Phe Arg Phe
 915 920

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAAGATT	CACTCCGCTT	TTTATTGATA	TCATTAGTAC	CTACGCTTTC	TATGTCGAAT	60
TTATTAGGAG	CTGCTACTAC	CGAACAGAGCTA	TCGGCTAGCA	ATAGCTTCGA	TGGAACCTACA	120
TCAACAAACAA	GCTTTCTAG	TAAAACATCA	TCGGCTACAG	ATGGCACCAA	TTATGTTTT	180
AAAGATTCTG	TAGTTATAGA	AAATGTACCC	AAAACAGGGG	AAACTCAGTC	TACTAGTTGT	240
TTTAAAAATG	ACGCTGCAGC	TGGAGATCTA	AATTCTTAG	GAGGGGGATT	TTCTTTCACA	300
TTTAGCAATA	TCGATGCAAC	CACGGCTTCT	GGAGCTGCTA	TTGGAAGTGA	AGCAGCTAAT	360
AAGACAGTCA	CGTTATCAGG	ATTTCGGCA	CTTCTTTTC	TTAAATCCCC	AGCAAGTACA	420
GTGACTAATG	GATTGGGAGC	TATCAATGTT	AAAGGGAATT	TAAGCCTATT	GGATAATGAT	480
AAGGTATTGA	TTCAGGACAA	TTCTCAACA	GGAGATGGCG	GAGCAATTAA	TTGTGCAGGC	540
TCCTTGAAGA	TCGCAACAA	TAAGTCCCCT	TCTTTTATTG	GAAATAGTTC	TTCAACACGTT	600
GGCGGAGCGA	TTCATACCAA	AAACCTCACA	CTATCTTCTG	GTGGGGAAAC	TCTATTTCAG	660
GGGAATACAG	CGCCTACGGC	TGCTGGTAAA	GGAGGTGCTA	TCGCGATTGC	AGACTCTGGC	720
ACCCCTATCCA	TTCTGGAGA	CACTGGCAGC	ATTATCTTG	AAGGCAATAC	GATAAGGAGCT	780
ACAGGAACCG	TCTCTCATAG	TGCTATTGAT	TTAGGAACTA	GCGCTAAGAT	AACTGCGTTA	840
CGTGCTGCGC	AAGGACATAC	GATATACTTT	TATGATCCGA	TTACTGTAAC	AGGATCGACA	900
TCTGTTGCTG	ATGCTCTCAA	TATTAATAGC	CCTGATACTG	GAGATAACAA	AGAGTATACG	960
GGAACCATAG	TCTTTCTGG	AGAGAACGTC	ACGGAGGCAG	AAGCTAAAGA	TGAGAACAC	1020
CGCACTTCTA	AATTACTTCA	AAATGTTGCT	TTTAAAATG	GGACTGTAGT	TTAAAAGGT	1080
GATGTCGTTT	TAAGTGCAGA	CGGTTCTCT	CAGGATGCAA	ACTCTAAGTT	GATTATGGAT	1140
TTAGGGACGT	CGTTGGTTGC	AAACACCGAA	AGTATCGAGT	TAACGAATT	GGAAATTAAT	1200
ATAGACTCTC	TCAGGAACGG	AAAAAAAGATA	AAACTCAGTG	CTGCCACAGC	TCAGAAAGAT	1260
ATTCGTATAG	ATCGTCTGT	TGTACTGGCA	ATTAGCGATG	AGAGTTTTA	TCAAAATGGC	1320
TTTTGAATG	AGGACCATTG	CTATGATGGG	ATTCTTGAGT	TAGATGCTGG	GAAAGACATC	1380
GTGATTTCTG	CAGATTCTCG	CAGTATAAT	GCTGTACAT	CTCCGTATGG	CTATCAGGG	1440
AAGTGGACAA	TCAATTGGTC	TACTGATGAT	AAGAAAGCTA	CGGTTCTTG	GGCAAAGCAA	1500
AGTTTTAATC	CCACTGCTGA	GCAGGAGGCT	CCGTTAGTTC	CTAATCTCT	TTGGGGTTCT	1560
TTTATAGATG	TTCGTCCTCT	CCAAAATT	ATAGAGCTAG	GTACTGAAGG	TGCTCCTTAC	1620
GAAAAGAGAT	TTTGGGTTGC	AGGCATTTCC	AATGTTTG	ATAGGAGCGG	TGGTAAAAT	1680
CAAAGGAAAT	TCCGTATGT	GAAGTGGAGGT	GCTGTAGTAG	GTGCTAGCAC	GAGGATGCCG	1740
GGTGGTGATA	CCTTGTCTCT	GGGTTTGCT	CAGCTCTTG	CGCGTACAA	AGACTACTTT	1800
ATGAATACCA	ATTTCGCAA	GACCTACGCA	GGATCTTAC	GTTCGAGCA	CGATGCTTCC	1860
CTATACTCTG	TGGTGAGTAT	CCTTTAGGA	GAGGGAGGAC	TCCGCGAGAT	CCTGTTGCCT	1920
TATGTTCCA	AGACTCTGCC	GTGCTCTTC	TATGGGCAGC	TTAGCTACGG	CCATACGGAT	1980
CATCGCATGA	AGACCGAGTC	TCTACCCCCC	CCCCCCCCGA	CGCTCTCGAC	GGATCATACT	2040
TCTTGGGGAG	GATATGTCTG	GGCTGGAGAG	CTGGGAAC	GAGTTGCTGT	TGAAAATACC	2100
AGCGGCAGAG	GATTTTCCG	AGAGTACACT	CCATTGTAA	AAGTCCAAGC	TGTTTACTCG	2160
CGCCAAGATA	GCTTTGTTGA	ACTAGGAGCT	ATCAGTCGT	ATTTTAGTGA	TTCGCATCTT	2220
TATAACCTTG	CGATTCCCT	TGGAATCAAG	TTAGAGAAC	GGTTTGCAGA	GCAATTATTAT	2280
CATGTTGTTAG	CGATGTATT	TCCAGATGTT	TGTCGTAGTA	ACCCCAAATG	TACGACTACC	2340
CTACTTCCA	ACCAAGGGAG	TTGGAAGACC	AAAGGTTCGA	ACTTAGCAAG	ACAGGCTGGT	2400

ATTGTTCAGG CCTCAGGTTT TCGATCTTG GGAGCTGCAG CAGAGCTTT CGGGAACTTT	2460
GGCTTGAAT GGCAGGGATC TTCTCGTAGC TATAATGTAG ATGCAGGTAG CAAAATCAA	2520
TTTTAG	2526

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 841 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Lys	Ile	Pro	Leu	Arg	Phe	Leu	Leu	Ile	Ser	Leu	Val	Pro	Thr	Leu
1				5					10				15		
Ser	Met	Ser	Asn	Leu	Leu	Gly	Ala	Ala	Thr	Thr	Glu	Glu	Leu	Ser	Ala
	20					25				30					
Ser	Asn	Ser	Phe	Asp	Gly	Thr	Thr	Ser	Thr	Thr	Ser	Phe	Ser	Ser	Lys
	35				40					45					
Thr	Ser	Ser	Ala	Thr	Asp	Gly	Thr	Asn	Tyr	Val	Phe	Lys	Asp	Ser	Val
	50				55				60						
Val	Ile	Glu	Asn	Val	Pro	Lys	Thr	Gly	Glu	Thr	Gln	Ser	Thr	Ser	Cys
	65				70				75			80			
Phe	Lys	Asn	Asp	Ala	Ala	Gly	Asp	Leu	Asn	Phe	Leu	Gly	Gly	Gly	
	85					90						95			
Phe	Ser	Phe	Thr	Phe	Ser	Asn	Ile	Asp	Ala	Thr	Thr	Ala	Ser	Gly	Ala
	100					105					110				
Ala	Ile	Gly	Ser	Glu	Ala	Ala	Asn	Lys	Thr	Val	Thr	Leu	Ser	Gly	Phe
	115					120				125					
Ser	Ala	Leu	Ser	Phe	Leu	Lys	Ser	Pro	Ala	Ser	Thr	Val	Thr	Asn	Gly
	130				135				140						
Leu	Gly	Ala	Ile	Asn	Val	Lys	Gly	Asn	Leu	Ser	Leu	Leu	Asp	Asn	Asp
	145				150				155			160			
Lys	Val	Leu	Ile	Gln	Asp	Asn	Phe	Ser	Thr	Gly	Asp	Gly	Gly	Ala	Ile
	165					170				175					
Asn	Cys	Ala	Gly	Ser	Leu	Lys	Ile	Ala	Asn	Asn	Lys	Ser	Leu	Ser	Phe
	180					185					190				
Ile	Gly	Asn	Ser	Ser	Ser	Thr	Arg	Gly	Gly	Ala	Ile	His	Thr	Lys	Asn
	195					200				205					
Leu	Thr	Leu	Ser	Ser	Gly	Gly	Glu	Thr	Leu	Phe	Gln	Gly	Asn	Thr	Ala
	210				215				220						

Pro Thr Ala Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly
 225 230 235 240
 Thr Leu Ser Ile Ser Gly Asp Ser Gly Asp Ile Ile Phe Glu Gly Asn
 245 250 255
 Thr Ile Gly Ala Thr Gly Thr Val Ser His Ser Ala Ile Asp Leu Gly
 260 265 270
 Thr Ser Ala Lys Ile Thr Ala Leu Arg Ala Ala Gln Gly His Thr Ile
 275 280 285
 Tyr Phe Tyr Asp Pro Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp
 290 295 300
 Ala Leu Asn Ile Asn Ser Pro Asp Thr Gly Asp Asn Lys Glu Tyr Thr
 305 310 315 320
 Gly Thr Ile Val Phe Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys
 325 330 335
 Asp Glu Lys Asn Arg Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys
 340 345 350
 Asn Gly Thr Val Val Leu Lys Gly Asp Val Val Leu Ser Ala Asn Gly
 355 360 365
 Phe Ser Gln Asp Ala Asn Ser Lys Leu Ile Met Asp Leu Gly Thr Ser
 370 375 380
 Leu Val Ala Asn Thr Glu Ser Ile Glu Leu Thr Asn Leu Glu Ile Asn
 385 390 395 400
 Ile Asp Ser Leu Arg Asn Gly Lys Ile Lys Leu Ser Ala Ala Thr
 405 410 415
 Ala Gln Lys Asp Ile Arg Ile Asp Arg Pro Val Val Leu Ala Ile Ser
 420 425 430
 Asp Glu Ser Phe Tyr Gln Asn Gly Phe Leu Asn Glu Asp His Ser Tyr
 435 440 445
 Asp Gly Ile Leu Glu Leu Asp Ala Gly Lys Asp Ile Val Ile Ser Ala
 450 455 460
 Asp Ser Arg Ser Ile Asn Ala Val Gln Ser Pro Tyr Gly Tyr Gln Gly
 465 470 475 480
 Lys Trp Thr Ile Asn Trp Ser Thr Asp Asp Lys Lys Ala Thr Val Ser
 485 490 495
 Trp Ala Lys Gln Ser Phe Asn Pro Thr Ala Glu Gln Glu Ala Pro Leu
 500 505 510
 Val Pro Asn Leu Leu Trp Gly Ser Phe Ile Asp Val Arg Pro Phe Gln
 515 520 525
 Asn Phe Ile Glu Leu Gly Thr Glu Gly Ala Pro Tyr Glu Lys Arg Phe

530	535	540
Trp Val Ala Gly Ile Ser Asn Val Leu His Arg Ser Gly Arg Glu Asn		
545	550	555
Gln Arg Lys Phe Arg His Val Ser Gly Gly Ala Val Val Gly Ala Ser		
565	570	575
Thr Arg Met Pro Gly Gly Asp Thr Leu Ser Leu Gly Phe Ala Gln Leu		
580	585	590
Phe Ala Arg Asp Lys Asp Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr		
595	600	605
Tyr Ala Gly Ser Leu Arg Leu Gln His Asp Ala Ser Leu Tyr Ser Val		
610	615	620
Val Ser Ile Leu Leu Gly Glu Gly Leu Arg Glu Ile Leu Leu Pro		
625	630	635
Tyr Val Ser Lys Thr Leu Pro Cys Ser Phe Tyr Gly Gln Leu Ser Tyr		
645	650	655
Gly His Thr Asp His Arg Met Lys Thr Glu Ser Leu Pro Pro Pro Pro		
660	665	670
Pro Thr Leu Ser Thr Asp His Thr Ser Trp Gly Gly Tyr Val Trp Ala		
675	680	685
Gly Glu Leu Gly Thr Arg Val Ala Val Glu Asn Thr Ser Gly Arg Gly		
690	695	700
Phe Phe Arg Glu Tyr Thr Pro Phe Val Lys Val Gln Ala Val Tyr Ser		
705	710	715
Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser		
725	730	735
Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu		
740	745	750
Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro		
755	760	765
Asp Val Cys Arg Ser Asn Pro Lys Cys Thr Thr Leu Leu Ser Asn		
770	775	780
Gln Gly Ser Trp Lys Thr Lys Gly Ser Asn Leu Ala Arg Gln Ala Gly		
785	790	795
Ile Val Gln Ala Ser Gly Phe Arg Ser Leu Gly Ala Ala Ala Glu Leu		
805	810	815
Phe Gly Asn Phe Gly Phe Glu Trp Arg Gly Ser Ser Arg Ser Tyr Asn		
820	825	830
Val Asp Ala Gly Ser Lys Ile Lys Phe		
835	840	

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2787 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAAGTCTT	CTTTCCCCAA	GTTTGTATT	TCTACATTTG	CTATTTCCC	TTTGTCTATG	60
ATTGCTACCG	AGACAGTTT	GGATTCAAGT	GCGAGTTCG	ATGGGAATAA	AAATGGTAAT	120
TTTCAGTTC	GTGAGAGTC	GGAAGATGCT	GGAACACTACCT	ACCTATTAA	GGGAAATGTC	180
ACTCTAGAAA	ATATTCTGG	AACAGGCACA	GCAATCACAA	AAAGCTGTT	TAACAACACT	240
AAGGGCGATT	TGACTTTCAC	AGGTAACGGG	AACTCTCTAT	TGTTCCAAAC	GGTGGATGCA	300
GGGACTGTAG	CAGGGCTGC	TGTTAACAGC	AGCGTGGTAG	ATAAATCTAC	CACGTTTATA	360
GGGTTTTCTT	CGCTATCTT	TATTGCGTCT	CCTGGAAGTT	CGATAACTAC	CGGCAAAGGA	420
GCCGTTAGCT	GCTCTACGGG	TAGCTTGAAG	TTTGACAAAAA	ATGTCAGTTT	GCTCTTCAGC	480
AAAAACTTTT	CAACGGATAA	TGGCGGTGCT	ATCACCGCAA	AAACTCTTTC	ATTAACAGGG	540
ACTACAATGT	CAGCTCTGTT	TTCTGAAAAT	ACCTCCTCAA	AGAAAAGCGG	AGCCATTCA	600
ACTTCCGATG	CCCTTACCAT	TACTGGAAAC	CAAGGGGAAG	TCTCTTTTC	TGACAATACT	660
TCTTCGGATT	CTGGAGCTGC	AATTTTACA	GAAGCCTCGG	TGACTATTTC	TAATAATGCT	720
AAAGTTTCCT	TTATTGACAA	TAAGGTACA	GGAGCGAGCT	CCTCAACAAAC	GGGGGATATG	780
TCAGGAGGTG	CTATCTGTGC	TTATAAAAAT	AGTACAGATA	CTAAGGTAC	CCTCACTGGA	840
AATCAGATGT	TACTCTTCAG	CAACAATACA	TCGACAAACAG	CGGGAGGAGC	TATCTATGTG	900
AAAAAGCTCG	AACTGGCTTC	CGGAGGACTT	ACCCATTTC	GTAGAAATAG	TGTCAATGGA	960
GGTACAGCTC	CTAAAGGTGG	AGCCATAGCT	ATCGAAGATA	GTGGGAAATT	GAGTTTATCC	1020
GCCGATAGTG	GTGACATTGT	CTTTTAGGG	AATACAGTC	CTTCTACTAC	TCTCTGGGACG	1080
AATAGAAGTA	GTATCGACTT	AGGAACGAGT	GCAAAGATGA	CAGCTTGCG	TTCTGCTGCT	1140
GGTAGAGCCA	TCTACTTCTA	TGATCCCAT	ACTACAGGAT	CTTCCACAAAC	AGTTACAGAT	1200
GTCTTAAAAG	TTAATGAGAC	TCCGGCAGAT	TCTGCACTAC	AATATACAGG	GAACATCATC	1260
TTCACAGGGAG	AAAAGTTATC	AGAGACAGAG	GCCGCAGATT	CTAAAAATCT	TACTTCGAAG	1320
CTACTACAGC	CTGTAACCT	TTCAGGAGGT	ACTCTATTT	TAAAACATGG	AGTGACTCTG	1380
CAGACTCAGG	CATTCACTCA	ACAGGCAGAT	TCTCGTCTCG	AAATGGACGT	AGGAACTACT	1440
CTAGAACCTG	CTGATACTAG	CACCATAAAC	AATTGGTCA	TTAACATCAG	TTCTATAGAC	1500
GGTCAAAGA	AGGCAAAAT	AGAAACCAA	GCTACGTCAA	AAAATCTGAC	TTTATCTGGA	1560
ACCATCACTT	TATTGGACCC	GACGGGCACG	TTTTATGAA	ATCATAGTT	AAGAAATCCT	1620
CAGTCCTACG	ACATCTTACA	GCTCAAAGCT	TCTGGAACTG	TAACAAGCAC	CGCAGTGACT	1680
CCAGATCCTA	TAATGGGTGA	GAATTCCAT	TACGGCTATC	AGGGAACCTG	GGGCCAAATT	1740
GTTCGGGGGA	CAGGGCTTC	TACGACTGCA	ACCTTCAC	GGACTAAAAC	TGCTATATT	1800
CCTAATCCCG	AGCGTATCGG	CTCTTTAGTC	CCTAATAGCT	TATGGAATGC	ATTATAGAT	1860
ATTAGCTCTC	TCCATTATCT	TATGGAGACT	GCAAACGAAG	GGTTGCAGGG	AGACCCTGCT	1920
TTTTGGTGTG	CTGGATTATC	TAACCTCTTC	CATAAGGATA	GTACAAAAAC	ACGACGCCGG	1980
TTTCGCCATT	TGAGTGGCGG	TTATGTCATA	GGAGGAAACC	TACATACTTG	TTCAAGATAAG	2040
ATTCTTAGTG	CTGCATTTTG	TCAGCTCTT	GGAAGAGATA	GAGACTACTT	TGTAGCTAAG	2100
AATCAAGGTA	CAGTCTACGG	AGGAACCTCTC	TATTACCGAC	ACAACGAAAC	CTATATCTCT	2160
CTTCCTTGCA	AACTACGGCC	TTGTTCGTTG	TCTTATGTTC	CTACAGAGAT	TCCTGTTCTC	2220
TTTTCAAGGAA	ACCTTAGCTA	CACCCATACG	GATAACGATC	TGAAAACCAA	GTATACAACA	2280
TATCCTACTG	TTAAAGGAAG	CTGGGGGAAT	GATAGTTCG	CTTTAGAATT	CGGTGGAAGA	2340
GCTCCGATT	GCTTAGATGA	AAGTGCTCTA	TTTGAGCAGT	ACATGCCCTT	CATGAAATTG	2400
CAGTTTGTCT	ATGCACATCA	GGAAAGGTTT	AAAGAACAGG	GAACAGAAC	TCGTGAATT	2460
GGAAGTAGCC	GTCTTGTGAA	TCTTGCCCTA	CCTATCGGGA	TCCGATTGTA	TAAGGAATCA	2520
GAATGCCAAG	ATGCAACGTA	CAATCTAACT	CTTGGTTATA	CTGTGGATCT	TGTTCGTAGT	2580
AACCCCGACT	GTACGACAAC	ACTGCGAATT	AGCGGTGATT	CTTGGAAAAC	CTTCGGTAGC	2640
AATTGGCAA	GACAAGCTT	AGTCCTCGT	GCAGGGAAACC	ATTTTGCTT	TAACTCAAAT	2700

TTTGAAGCCT TTAGCCAATT TTCTTTGAA TTGCGTGGGT CATCTCGCAA TTACAATGTA	2760
GACTTAGGAG CAAAATACCA ATTCTAA	2787

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys Ser Ser Phe Pro Lys Phe Val Phe Ser Thr Phe Ala Ile Phe			
1	5	10	15

Pro Leu Ser Met Ile Ala Thr Glu Thr Val Leu Asp Ser Ser Ala Ser		
20	25	30

Phe Asp Gly Asn Lys Asn Gly Asn Phe Ser Val Arg Glu Ser Gln Glu		
35	40	45

Asp Ala Gly Thr Thr Tyr Leu Phe Lys Gly Asn Val Thr Leu Glu Asn		
50	55	60

Ile Pro Gly Thr Gly Thr Ala Ile Thr Lys Ser Cys Phe Asn Asn Thr			
65	70	75	80

Lys Gly Asp Leu Thr Phe Thr Gly Asn Gly Asn Ser Leu Leu Phe Gln		
85	90	95

Thr Val Asp Ala Gly Thr Val Ala Gly Ala Ala Val Asn Ser Ser Val		
100	105	110

Val Asp Lys Ser Thr Thr Phe Ile Gly Phe Ser Ser Leu Ser Phe Ile		
115	120	125

Ala Ser Pro Gly Ser Ser Ile Thr Thr Gly Lys Gly Ala Val Ser Cys		
130	135	140

Ser Thr Gly Ser Leu Lys Phe Asp Lys Asn Val Ser Leu Leu Phe Ser			
145	150	155	160

Lys Asn Phe Ser Thr Asp Asn Gly Gly Ala Ile Thr Ala Lys Thr Leu		
165	170	175

Ser Leu Thr Gly Thr Thr Met Ser Ala Leu Phe Ser Glu Asn Thr Ser		
180	185	190

Ser Lys Lys Gly Gly Ala Ile Gln Thr Ser Asp Ala Leu Thr Ile Thr		
195	200	205

Gly Asn Gln Gly Glu Val Ser Phe Ser Asp Asn Thr Ser Ser Asp Ser		
210	215	220

Gly Ala Ala Ile Phe Thr Glu Ala Ser Val Thr Ile Ser Asn Asn Ala	
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225	230	235	240
Lys Val Ser Phe Ile Asp Asn Lys Val Thr Gly Ala Ser Ser Ser Thr			
245		250	255
Thr Gly Asp Met Ser Gly Gly Ala Ile Cys Ala Tyr Lys Thr Ser Thr			
260	265	270	
Asp Thr Lys Val Thr Leu Thr Gly Asn Gln Met Leu Leu Phe Ser Asn			
275	280	285	
Asn Thr Ser Thr Thr Ala Gly Gly Ala Ile Tyr Val Lys Lys Leu Glu			
290	295	300	
Leu Ala Ser Gly Gly Leu Thr Leu Phe Ser Arg Asn Ser Val Asn Gly			
305	310	315	320
Gly Thr Ala Pro Lys Gly Gly Ala Ile Ala Ile Glu Asp Ser Gly Glu			
325	330	335	
Leu Ser Leu Ser Ala Asp Ser Gly Asp Ile Val Phe Leu Gly Asn Thr			
340	345	350	
Val Thr Ser Thr Thr Pro Gly Thr Asn Arg Ser Ser Ile Asp Leu Gly			
355	360	365	
Thr Ser Ala Lys Met Thr Ala Leu Arg Ser Ala Ala Gly Arg Ala Ile			
370	375	380	
Tyr Phe Tyr Asp Pro Ile Thr Thr Gly Ser Ser Thr Thr Val Thr Asp			
385	390	395	400
Val Leu Lys Val Asn Glu Thr Pro Ala Asp Ser Ala Leu Gln Tyr Thr			
405	410	415	
Gly Asn Ile Ile Phe Thr Gly Glu Lys Leu Ser Glu Thr Glu Ala Ala			
420	425	430	
Asp Ser Lys Asn Leu Thr Ser Lys Leu Leu Gln Pro Val Thr Leu Ser			
435	440	445	
Gly Gly Thr Leu Ser Leu Lys His Gly Val Thr Leu Gln Thr Gln Ala			
450	455	460	
Phe Thr Gln Gln Ala Asp Ser Arg Leu Glu Met Asp Val Gly Thr Thr			
465	470	475	480
Leu Glu Pro Ala Asp Thr Ser Thr Ile Asn Asn Leu Val Ile Asn Ile			
485	490	495	
Ser Ser Ile Asp Gly Ala Lys Lys Ala Lys Ile Glu Thr Lys Ala Thr			
500	505	510	
Ser Lys Asn Leu Thr Leu Ser Gly Thr Ile Thr Leu Leu Asp Pro Thr			
515	520	525	
Gly Thr Phe Tyr Glu Asn His Ser Leu Arg Asn Pro Gln Ser Tyr Asp			
530	535	540	

Ile Leu Glu Leu Lys Ala Ser Gly Thr Val Thr Ser Thr Ala Val Thr
 545 550 555 560

Pro Asp Pro Ile Met Gly Glu Lys Phe His Tyr Gly Tyr Gln Gly Thr
 565 570 575

Trp Gly Pro Ile Val Trp Gly Thr Gly Ala Ser Thr Thr Ala Thr Phe
 580 585 590

Asn Trp Thr Lys Thr Gly Tyr Ile Pro Asn Pro Glu Arg Ile Gly Ser
 595 600 605

Leu Val Pro Asn Ser Leu Trp Asn Ala Phe Ile Asp Ile Ser Ser Leu
 610 615 620

His Tyr Leu Met Glu Thr Ala Asn Glu Gly Leu Gln Gly Asp Arg Ala
 625 630 635 640

Phe Trp Cys Ala Gly Leu Ser Asn Phe Phe His Lys Asp Ser Thr Lys
 645 650 655

Thr Arg Arg Gly Phe Arg His Leu Ser Gly Gly Tyr Val Ile Gly Gly
 660 665 670

Asn Leu His Thr Cys Ser Asp Lys Ile Leu Ser Ala Ala Phe Cys Gln
 675 680 685

Leu Phe Gly Arg Asp Arg Asp Tyr Phe Val Ala Lys Asn Gln Gly Thr
 690 695 700

Val Tyr Gly Gly Thr Leu Tyr Tyr Gln His Asn Glu Thr Tyr Ile Ser
 705 710 715 720

Leu Pro Cys Lys Leu Arg Pro Cys Ser Leu Ser Tyr Val Pro Thr Glu
 725 730 735

Ile Pro Val Leu Phe Ser Gly Asn Leu Ser Tyr Thr His Thr Asp Asn
 740 745 750

Asp Leu Lys Thr Lys Tyr Thr Thr Tyr Pro Thr Val Lys Gly Ser Trp
 755 760 765

Gly Asn Asp Ser Phe Ala Leu Glu Phe Gly Gly Arg Ala Pro Ile Cys
 770 775 780

Leu Asp Glu Ser Ala Leu Phe Glu Gln Tyr Met Pro Phe Met Lys Leu
 785 790 795 800

Gln Phe Val Tyr Ala His Gln Glu Gly Phe Lys Glu Gln Gly Thr Glu
 805 810 815

Ala Arg Glu Phe Gly Ser Ser Arg Leu Val Asn Leu Ala Leu Pro Ile
 820 825 830

Gly Ile Arg Phe Asp Lys Glu Ser Asp Cys Gln Asp Ala Thr Tyr Asn
 835 840 845

Leu Thr Leu Gly Tyr Thr Val Asp Leu Val Arg Ser Asn Pro Asp Cys
 850 855 860

Thr Thr Thr Leu Arg Ile Ser Gly Asp Ser Trp Lys Thr Phe Gly Thr
 865 870 875 880

Asn Leu Ala Arg Gln Ala Leu Val Leu Arg Ala Gly Asn His Phe Cys
 885 890 895

Phe Asn Ser Asn Phe Glu Ala Phe Ser Gln Phe Ser Phe Glu Leu Arg
 900 905 910

Gly Ser Ser Arg Asn Tyr Asn Val Asp Leu Gly Ala Lys Tyr Gln Phe
 915 920 925

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAGATCGT	CTTTTCCTT	GTTATTATA	TCTTCATCTC	TAGCCTTCC	TCTCTTAATG	60
AGTGTTCCTG	CAGATGCTGC	CGATCTACA	TTAGGGAGTC	GTGACAGTTA	TAATGGTGT	120
ACAAGCACCA	CAGAATTAC	TCCTAAAGCG	GCAACTTCTG	ATGCTAGTGG	CACGACCTAT	180
ATTCTCGATG	GGGATGTCTC	GATAAGCCAA	GCAGGGAAAC	AAACGAGCTT	AACCACAAGT	240
TGTTTTCTA	ACACTGCAGG	AAATCTTAC	TTCTTAGGGA	ACGGATTTC	TCTTCATTTC	300
GACAATATTA	TTTCGCTAC	TGTTGCAGGT	GTTGTTGTTA	GCAATACAGC	AGCTTCTGGG	360
ATTACGAAAT	TCTCAGGATT	TCACAACCTT	CGGATGCTTG	CAGCTCTAG	GACCACAGGT	420
AAAGGAGCCA	TTAAAATTAC	CGATGGTCTG	GTGTTTGAGA	GTATAGGGAA	TCTTGACCAA	480
AATGAAAATG	CCTCTAGTGA	AAATGGGGA	GCCATCAATA	CGAACAGCTT	GTCTTTGACT	540
GGGAGTACGC	GGTTTGTAGC	GTTCCTTGGC	AATAGCTCGT	CGCAACAAAG	GGGAGCGATC	600
TATGCTCTG	GTGACTCTGT	GATTCTGAG	AATGCAGGAA	TCTTGAGCTT	CGGAAACAAAC	660
AGTGCACAA	CATCAGGAGG	CGCGATCTCT	GCTGAAGGGA	ACCTTGTGAT	CTCCAATAAC	720
CAAAATATCT	TTTCGATGG	CTGCAAAGCA	ACTACAAATG	CGGGAGCTAT	TGATTGTAAC	780
AAAGCAGGGG	CGAACCCAGA	CCCTATCTG	ACTCTTCAG	GAAATGAGAG	CCTGCATTTC	840
CTGAATAACA	CAGCAGGAAA	TAGTGGAGGT	GCGATTATA	CCAAAAAAATT	GGTGTATCC	900
TCAGGACGAG	GAGGAGTGT	ATTTCTAAC	AACAAAGCTG	CGAATGCTAC	TCTAAAGGA	960
GGGGCAATTG	CGATTCTAGA	TTCTGGAGAG	ATTAGCATT	CTGCAGATCT	CGCAATATC	1020
ATTTTCGAGG	GCAAACTAC	GAGCACTACA	GGAAAGTCTG	CGAGTGTGAC	CAGAAATGCT	1080
ATAGATCTTG	CATCGAATGC	AAAATTCTTA	AATCTCCGAG	CGACTCGGGG	AAATAAAGTT	1140
ATTTTCATG	ATCCTATCAC	GAGCTCAGGA	GCTACTGATA	AGCTCTCTT	GAATAAAGCT	1200
GACGCAGGAT	CTGGAAATAC	CTATGAAGGC	TACATCGTT	TCTCTGGAGA	GAAACTCTCA	1260
GAAGAGGAAC	TTAAGAAACC	TGACAATCTG	AAGTCTACAT	TTACACAGGC	TGTAGAGCTT	1320
GCTGCAGGTG	CCTTAGTATT	GAAAGATGGA	GTGACTGTAG	TTGCAAATAC	TATAACGCAG	1380
GTCGAGGGAT	CGAAAGTCGT	TATGGATGGA	GGGACTACTT	TTGAGGCAAG	CGCTGAGGGG	1440
GTCACTCTCA	ATGGCCTAGC	CATTAATATA	GATTCTTAG	ATGGGACAAA	TAAAGCTATC	1500
ATTAAGGCGA	CGGCAGCAAG	TAAGGATGTT	GCCTTATCG	GGCCTATCAT	GCTTGTAGAT	1560
GCTCAGGGGA	ACTATTATGA	GCATCATATA	CTCAGTCAC	AGCAGGTCTT	TCCTTTAATA	1620
GAGCTTTCTG	CACAAGGAAC	GATGACTACT	ACAGATATCC	CCGATACCCC	AATTCTAAAT	1680
ACTACGAATC	ACTATGGGTA	TCAAGGAACT	GGAATAATTG	TTTGGGTCGA	CGATGCAACT	1740
GCAAAACAA	AAAATGCTAC	CTTAACTTGG	ACTAAAACAG	GATACAAGCC	GAATCCAGAA	1800
CGTCAGGGAC	CTTGGTTCC	TAATAGCCTG	TGGGGTTCTT	TTGTCGATGT	CCGCTCCATT	1860

CAGAGCCTCA	TGGACCGGAG	CACAAGTCG	TTATCTCGT	CAACAAATT	GTGGGTATCA	1920
GGAATCGCGG	ACTTTTGCA	TGAAGATCAG	AAAGGAAACC	AACGTAGTTA	TCGTCATTCT	1980
ACCGCGGGTT	ATGCATTAGG	AGGAGGATTC	TTCACGGCTT	CTGAAAATT	CTTTAATT	2040
GCTTTTGTC	AGCTTTGAG	CTACGACAAG	GACCACCTTG	TGGCTAAGAA	CCATAACCAT	2100
GTATATGCAG	GGGCAATGAG	TTACCGACAC	CTCGGAGAGT	CTAACACCCT	CGCTAACATT	2160
TTGTCAGGAA	ATTCTGACTC	CCTACCTTT	GTCTTCATG	CTCGGTTTGC	TTATGGCCAT	2220
ACCGACAATA	ACATGACCAAC	AAAGTACACT	GGCTATTCTC	CTGTTAAGGG	AAGCTGGGA	2280
AATGATGCCT	TCGGTATAGA	ATGTGGAGGA	GCTATCCCAG	TAGTTGCTTC	AGGACGTCGG	2340
TCTTGGGTGG	ATACCCACAC	GCCATTTCTA	AACCTAGAGA	TGATCTATGC	ACATCAGAAT	2400
GACTTTAAGG	AAAACGGCAC	AGAAGGCCGT	TCTTCCAAA	GTGAAGACCT	CTTCAATCTA	2460
GCGGTTCCCTG	TAGGGATAAA	ATTTGAGAAA	TTCTCCGATA	AGTCTACGTA	TGATCTCTCC	2520
ATAGCTTACG	TTCCCGATGT	GATTCTGTAAT	GATCCAGGCT	GCACGACAAC	TCTTATGGTT	2580
TCTGGGGATT	CTTGGTCGAC	ATGTGGTACA	AGCTTGTCTA	GACAAGCTCT	TCTTGTACGT	2640
GCTGGAAATC	ATCATGCCTT	TGCTTCAAAC	TTTGAAGTTT	TCAGTCAGTT	TGAAGTCGAG	2700
TTGCGAGGTT	CTTCTCGTAG	CTATGCTATC	GATCTGGAG	GAAGATTCTGG	ATTTTAA	2757

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 918 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Arg	Ser	Ser	Phe	Ser	Leu	Leu	Leu	Ile	Ser	Ser	Ser	Leu	Ala	Phe
1					5				10				15		
Pro	Leu	Leu	Met	Ser	Val	Ser	Ala	Asp	Ala	Ala	Asp	Leu	Thr	Leu	Gly
					20				25				30		
Ser	Arg	Asp	Ser	Tyr	Asn	Gly	Asp	Thr	Ser	Thr	Thr	Glu	Phe	Thr	Pro
					35				40				45		
Lys	Ala	Ala	Thr	Ser	Asp	Ala	Ser	Gly	Thr	Thr	Tyr	Ile	Leu	Asp	Gly
					50				55				60		
Asp	Val	Ser	Ile	Ser	Gln	Ala	Gly	Lys	Gln	Thr	Ser	Leu	Thr	Thr	Ser
					65				70				75		80
Cys	Phe	Ser	Asn	Thr	Ala	Gly	Asn	Leu	Thr	Phe	Leu	Gly	Asn	Gly	Phe
					85				90				95		
Ser	Leu	His	Phe	Asp	Asn	Ile	Ile	Ser	Ser	Thr	Val	Ala	Gly	Val	Val
					100				105				110		
Val	Ser	Asn	Thr	Ala	Ala	Ser	Gly	Ile	Thr	Lys	Phe	Ser	Gly	Phe	Ser
					115				120				125		
Thr	Leu	Arg	Met	Leu	Ala	Ala	Pro	Arg	Thr	Thr	Gly	Lys	Gly	Ala	Ile
					130				135				140		
Lys	Ile	Thr	Asp	Gly	Leu	Val	Phe	Glu	Ser	Ile	Gly	Asn	Leu	Asp	Gln
					145				150				155		160

Asn Glu Asn Ala Ser Ser Glu Asn Gly Gly Ala Ile Asn Thr Lys Thr
 165 170 175

Leu Ser Leu Thr Gly Ser Thr Arg Phe Val Ala Phe Leu Gly Asn Ser
 180 185 190

Ser Ser Gln Gln Gly Gly Ala Ile Tyr Ala Ser Gly Asp Ser Val Ile
 195 200 205

Ser Glu Asn Ala Gly Ile Leu Ser Phe Gly Asn Asn Ser Ala Thr Thr
 210 215 220

Ser Gly Gly Ala Ile Ser Ala Glu Gly Asn Leu Val Ile Ser Asn Asn
 225 230 235 240

Gln Asn Ile Phe Phe Asp Gly Cys Lys Ala Thr Thr Asn Gly Gly Ala
 245 250 255

Ile Asp Cys Asn Lys Ala Gly Ala Asn Pro Asp Pro Ile Leu Thr Leu
 260 265 270

Ser Gly Asn Glu Ser Leu His Phe Leu Asn Asn Thr Ala Gly Asn Ser
 275 280 285

Gly Gly Ala Ile Tyr Thr Lys Lys Leu Val Leu Ser Ser Gly Arg Gly
 290 295 300

Gly Val Leu Phe Ser Asn Asn Lys Ala Ala Asn Ala Thr Pro Lys Gly
 305 310 315 320

Gly Ala Ile Ala Ile Leu Asp Ser Gly Glu Ile Ser Ile Ser Ala Asp
 325 330 335

Leu Gly Asn Ile Ile Phe Glu Gly Asn Thr Thr Ser Thr Thr Gly Ser
 340 345 350

Pro Ala Ser Val Thr Arg Asn Ala Ile Asp Leu Ala Ser Asn Ala Lys
 355 360 365

Phe Leu Asn Leu Arg Ala Thr Arg Gly Asn Lys Val Ile Phe Tyr Asp
 370 375 380

Pro Ile Thr Ser Ser Gly Ala Thr Asp Lys Leu Ser Leu Asn Lys Ala
 385 390 395 400

Asp Ala Gly Ser Gly Asn Thr Tyr Glu Gly Tyr Ile Val Phe Ser Gly
 405 410 415

Glu Lys Leu Ser Glu Glu Glu Leu Lys Lys Pro Asp Asn Leu Lys Ser
 420 425 430

Thr Phe Thr Gln Ala Val Glu Leu Ala Ala Gly Ala Leu Val Leu Lys
 435 440 445

Asp Gly Val Thr Val Val Ala Asn Thr Ile Thr Gln Val Glu Gly Ser
 450 455 460

Lys Val Val Met Asp Gly Gly Thr Thr Phe Glu Ala Ser Ala Glu Gly

465	470	475	480
Val Thr Leu Asn Gly Leu Ala Ile Asn Ile Asp Ser Leu Asp Gly Thr			
485		490	495
Asn Lys Ala Ile Ile Lys Ala Thr Ala Ala Ser Lys Asp Val Ala Leu			
500	505	510	
Ser Gly Pro Ile Met Leu Val Asp Ala Gln Gly Asn Tyr Tyr Glu His			
515	520	525	
His Asn Leu Ser Gln Gln Val Phe Pro Leu Ile Glu Leu Ser Ala			
530	535	540	
Gln Gly Thr Met Thr Thr Asp Ile Pro Asp Thr Pro Ile Leu Asn			
545	550	555	560
Thr Thr Asn His Tyr Gly Tyr Gln Gly Thr Gly Ile Ile Val Trp Val			
565	570	575	
Asp Asp Ala Thr Ala Lys Thr Lys Asn Ala Thr Leu Thr Trp Thr Lys			
580	585	590	
Thr Gly Tyr Lys Pro Asn Pro Glu Arg Gln Gly Pro Leu Val Pro Asn			
595	600	605	
Ser Leu Trp Gly Ser Phe Val Asp Val Arg Ser Ile Gln Ser Leu Met			
610	615	620	
Asp Arg Ser Thr Ser Ser Leu Ser Ser Ser Thr Asn Leu Trp Val Ser			
625	630	635	640
Gly Ile Ala Asp Phe Leu His Glu Asp Gln Lys Gly Asn Gln Arg Ser			
645	650	655	
Tyr Arg His Ser Ser Ala Gly Tyr Ala Leu Gly Gly Phe Phe Thr			
660	665	670	
Ala Ser Glu Asn Phe Phe Asn Phe Ala Phe Cys Gln Leu Phe Gly Tyr			
675	680	685	
Asp Lys Asp His Leu Val Ala Lys Asn His Thr His Val Tyr Ala Gly			
690	695	700	
Ala Met Ser Tyr Arg His Leu Gly Glu Ser Lys Thr Leu Ala Lys Ile			
705	710	715	720
Leu Ser Gly Asn Ser Asp Ser Leu Pro Phe Val Phe Asn Ala Arg Phe			
725	730	735	
Ala Tyr Gly His Thr Asp Asn Asn Met Thr Thr Lys Tyr Thr Gly Tyr			
740	745	750	
Ser Pro Val Lys Gly Ser Trp Gly Asn Asp Ala Phe Gly Ile Glu Cys			
755	760	765	
Gly Gly Ala Ile Pro Val Val Ala Ser Gly Arg Arg Ser Trp Val Asp			
770	775	780	

Thr His Thr Pro Phe Leu Asn Leu Glu Met Ile Tyr Ala His Gln Asn
 785 790 795 800

Asp Phe Lys Glu Asn Gly Thr Glu Gly Arg Ser Phe Gln Ser Glu Asp
 805 810 815

Leu Phe Asn Leu Ala Val Pro Val Gly Ile Lys Phe Glu Lys Phe Ser
 820 825 830

Asp Lys Ser Thr Tyr Asp Leu Ser Ile Ala Tyr Val Pro Asp Val Ile
 835 840 845

Arg Asn Asp Pro Gly Cys Thr Thr Leu Met Val Ser Gly Asp Ser
 850 855 860

Trp Ser Thr Cys Gly Thr Ser Leu Ser Arg Gln Ala Leu Leu Val Arg
 865 870 875 880

Ala Gly Asn His His Ala Phe Ala Ser Asn Phe Glu Val Phe Ser Gln
 885 890 895

Phe Glu Val Glu Leu Arg Gly Ser Ser Arg Ser Tyr Ala Ile Asp Leu
 900 905 910

Gly Gly Arg Phe Gly Phe
 915

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2787 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGAAATCCT	CTCTTCATTG	GTTTGTAAATC	TCGTCATCTT	TAGCACTTCC	CTTGTCACTA	60
AATTTCCTCTG	CGTTTGCTGC	TGTTGTTGAA	ATCAATCTAG	GACCTACCAA	TAGCTTCTCT	120
GGACCAGGAA	CCTACACTCC	TCCAGCCCCAA	ACAACAAATG	CAGATGGAAC	TATCTATAAT	180
CTAACAGGGG	ATGTCCTAAT	CACCAATGCA	GGATCTCCGA	CAGCTCTAAC	CGCTTCCTGC	240
TTTAAAGAAA	CTACTGGGAA	TCTTCTTTC	CAAGGCCACG	GCTACCAATT	TCTCCTACAA	300
AATATCGATG	CGGGAGCGAA	CTGTACCTT	ACCAATACAG	CTGCAAATAA	GCTTCTCTCC	360
TTTCAGGAT	TCTCCATT	GTCACTAATA	CAAACCACGA	ATGCTCACAC	AGGAACAGGA	420
GCCATCAAGT	CCACAGGAGC	TGTTCTATT	CAGTCGAACT	ATAGTTGCTA	CTTGGCCAA	480
AACTTTCTA	ATGACAATGG	AGGCGCCCTC	CAAGGCAGCT	CTATCAGTCT	ATCGCTAAC	540
CCCAACCTAA	CGTTGCCAA	AAACAAAGCA	ACGCAAAAG	GGGGTGCCCT	CTATTCCACG	600
GGAGGGATTA	CAATTAACAA	TACGTTAAC	TCAGCATCAT	TTTCTGAAAA	TACCGCGGCG	660
AACAATGGCG	GAGCCATT	CACGGAAGCT	AGCAGTTTA	TTAGCAGCAA	CAAAGCAATT	720
AGCTTATATA	ACAATAGTGT	GACCGCAACC	TCAGCTACAG	GGGGAGCCAT	TTACTGTAGT	780
AGTACATCAG	CCCCCAAACC	AGTCTTAAC	CTATCAGACA	ACGGGAACT	GAACTTTATA	840
GGAAATACAG	CAATTACTAG	TGGTGGGGCG	ATTTATACTG	ACAATCTAGT	TCTTCTTCT	900
GGAGGACCTA	CGCTTTTAA	AAACAACTCT	GCTATAGATA	CTGCAGCTCC	CTTAGGAGGA	960
GCAATTGCGA	TTGCTGACTC	TGGATCTTG	AGTCTTCGG	CTCTTGGTGG	AGACATCACT	1020
TTTGAAGGAA	ACACAGTAGT	CAAAGGAGCT	TCTTCGAGTC	AGACCACTAC	CAGAAATTCT	1080

ATTAACATCG	GAAACACCAA	TGCTAAGATT	GTACAGCTGC	GAGCCTCTCA	AGGCAATACT	1140
ATCTACTTCT	ATGATCCTAT	AACAACATAC	CATACTGCAG	CTCTCTCAGA	TGCTCTAAAC	1200
TTAAATGGTC	CTGACCTTGC	AGGGAAATCCT	GCATATCAAG	GAACCATCGT	ATTTCAGCAA	1260
GAGAAGCTCT	CGGAAGCAGA	AGCTGCAGAA	GCTGATAATC	TCAAATCTAC	AATTCAAG	1320
CCTCTAACTC	TTGCAGGGAGG	GCAACTCTCT	CTTAAATCAG	GAGTCACTCT	AGTGCTAAG	1380
TCCTTTCGC	AATCTCCGGG	CTCTACCCCTC	CTCATGGATG	CAGGGACCAC	ATTAGAAACC	1440
GCTGATGGGA	TCACTATCAA	TAATCTTGTG	CTCAATGTAG	ATTCCTTAAA	AGAGACCAAG	1500
AAGGCTACGC	AAAAAGCAAC	ACAAGCAAGT	CAGACAGTCA	CTTTATCTGG	ATCGCTCTCT	1560
CTTGTAGATC	CTTCTGGAAA	TGTCTACGAA	GATGTCTCTT	GGAATAACCC	TCAAGTCTTT	1620
TCTTGTCTCA	CTCTTACTGC	TGACGACCCC	GCGAATATTG	ACATCACAGA	CTTAGCTGCT	1680
GATCCCCTAG	AAAAAAATCC	TATCCATTGG	GGATACCAAG	GGAATTGGGC	ATTATCTTGG	1740
CAAGAGGATA	CTGCGACTAA	ATCCAAAGCA	GCGACTCTTA	CCTGGACAAA	AAACAGGATAC	1800
AATCCGAATC	CTGAGCGTCG	TGGAACCTTA	GTTGCTAAC	CGCTATGGGG	ATCCTTTGTT	1860
GATGTGCGCT	CCATACAACA	GCTTGTAGCC	ACTAAAGTAC	GCCAATCTCA	AGAAACTCGC	1920
GGCATCTGGT	GTGAGGGAT	CTCGAACTTC	TTCCATATAAG	ATAGCACGAA	GATAAATAAA	1980
GGTTTCGCC	ACATAAGTGC	AGGTTATGTT	GTAGGAGCGA	CTACAAACATT	AGCTTCTGAT	2040
AATCTTATCA	CTGCAGCCTT	CTGCCAATT	TTCGGGAAAG	ATAGAGATCA	CTTTATAAAT	2100
AAAAAATAGAG	CTTCTGCCTA	TGCAAGCTCT	CTCCATCTCC	AGCATCTAGC	GACCTTGTCT	2160
TCTCCAAGCT	TGTTACGCTA	CCTTCCTGGA	TCTGAAAGTG	AGCAGCCTGT	CCTCTTTGAT	2220
GCTCAGATCA	GCTATATCTA	TAGTAAAAAT	ACTATGAAAAA	CCTATTACAC	CCAAGCACCA	2280
AAGGGAGAGA	GCTCGTGGTA	TAATGACGGT	TGCGCTCTGG	AACTTGCAG	CTCCCTACCA	2340
CACACTGCTT	TAAGCCATGA	GGGTCTCTTC	CACCGTATT	TTCCCTTCAT	CAAAGTAGAA	2400
GCTTCGTA	TACACCAAGA	TAGCTTCAA	GAACGTAATA	CTACCTTGGT	ACGATCTTTC	2460
GATAGCGGTG	ATTTAATTAA	CGTCTCTGTG	CCTATTGGAA	TTACCTTCGA	GAGATTCTCG	2520
AGAAACGAGC	GTGCGCTTTA	CGAAGCTACT	GTCATCTACG	TTGCCGATGT	CTATCGTAAG	2580
AATCCTGACT	GCACGACAGC	TCTCCTAAATC	AAACAATACCT	CGTGGAAAAC	TACAGGAACG	2640
AATCTCTCAA	GACAAGCTGG	TATCGGAAGA	GCAGGGATCT	TTTATGCCTT	CTCTCCAAAT	2700
CTTGAGGTCA	CAAGTAACCT	ATCTATGGAA	ATTGTTGGAT	CTTCACGCAG	CTACAATGCA	2760
GATCTTGGAG	GTAAGTTCCA	GTTCTAA				2787

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Lys	Ser	Ser	Leu	His	Trp	Phe	Val	Ile	Ser	Ser	Ser	Leu	Ala	Leu
1				5					10				15		

Pro	Leu	Ser	Leu	Asn	Phe	Ser	Ala	Phe	Ala	Ala	Val	Val	Glu	Ile	Asn
				20				25				30			

Leu	Gly	Pro	Thr	Asn	Ser	Phe	Ser	Gly	Pro	Gly	Thr	Tyr	Thr	Pro	Pro
				35			40				45				

Ala	Gln	Thr	Thr	Asn	Ala	Asp	Gly	Thr	Ile	Tyr	Asn	Leu	Thr	Gly	Asp
				50			55			60					

Val	Ser	Ile	Thr	Asn	Ala	Gly	Ser	Pro	Thr	Ala	Leu	Thr	Ala	Ser	Cys
				65			70		75				80		

Phe	Lys	Glu	Thr	Thr	Gly	Asn	Leu	Ser	Phe	Gln	Gly	His	Gly	Tyr	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85	90	95
Phe Leu Leu Gln Asn Ile Asp Ala Gly Ala Asn Cys Thr Phe Thr Asn		
100	105	110
Thr Ala Ala Asn Lys Leu Leu Ser Phe Ser Gly Phe Ser Tyr Leu Ser		
115	120	125
Leu Ile Gln Thr Thr Asn Ala Thr Thr Gly Thr Gly Ala Ile Lys Ser		
130	135	140
Thr Gly Ala Cys Ser Ile Gln Ser Asn Tyr Ser Cys Tyr Phe Gly Gln		
145	150	155
Asn Phe Ser Asn Asp Asn Gly Gly Ala Leu Gln Gly Ser Ser Ile Ser		
165	170	175
Leu Ser Leu Asn Pro Asn Leu Thr Phe Ala Lys Asn Lys Ala Thr Gln		
180	185	190
Lys Gly Gly Ala Leu Tyr Ser Thr Gly Gly Ile Thr Ile Asn Asn Thr		
195	200	205
Leu Asn Ser Ala Ser Phe Ser Glu Asn Thr Ala Ala Asn Asn Gly Gly		
210	215	220
Ala Ile Tyr Thr Glu Ala Ser Ser Phe Ile Ser Ser Asn Lys Ala Ile		
225	230	235
Ser Phe Ile Asn Asn Ser Val Thr Ala Thr Ser Ala Thr Gly Gly Ala		
245	250	255
Ile Tyr Cys Ser Ser Thr Ser Ala Pro Lys Pro Val Leu Thr Leu Ser		
260	265	270
Asp Asn Gly Glu Leu Asn Phe Ile Gly Asn Thr Ala Ile Thr Ser Gly		
275	280	285
Gly Ala Ile Tyr Thr Asp Asn Leu Val Leu Ser Ser Gly Gly Pro Thr		
290	295	300
Leu Phe Lys Asn Asn Ser Ala Ile Asp Thr Ala Ala Pro Leu Gly Gly		
305	310	315
Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser Leu Ser Ala Leu Gly		
325	330	335
Gly Asp Ile Thr Phe Glu Gly Asn Thr Val Val Lys Gly Ala Ser Ser		
340	345	350
Ser Gln Thr Thr Arg Asn Ser Ile Asn Ile Gly Asn Thr Asn Ala		
355	360	365
Lys Ile Val Gln Leu Arg Ala Ser Gln Gly Asn Thr Ile Tyr Phe Tyr		
370	375	380
Asp Pro Ile Thr Thr Asn His Thr Ala Ala Leu Ser Asp Ala Leu Asn		
385	390	400

Leu Asn Gly Pro Asp Leu Ala Gly Asn Pro Ala Tyr Gln Gly Thr Ile
 405 410 415

Val Phe Ser Gly Glu Lys Leu Ser Glu Ala Glu Ala Ala Glu Ala Asp
 420 425 430

Asn Leu Lys Ser Thr Ile Gln Gln Pro Leu Thr Leu Ala Gly Gly Gln
 435 440 445

Leu Ser Leu Lys Ser Gly Val Thr Leu Val Ala Lys Ser Phe Ser Gln
 450 455 460

Ser Pro Gly Ser Thr Leu Leu Met Asp Ala Gly Thr Thr Leu Glu Thr
 465 470 475 480

Ala Asp Gly Ile Thr Ile Asn Asn Leu Val Leu Asn Val Asp Ser Leu
 485 490 495

Lys Glu Thr Lys Lys Ala Thr Leu Lys Ala Thr Gln Ala Ser Gln Thr
 500 505 510

Val Thr Leu Ser Gly Ser Leu Ser Leu Val Asp Pro Ser Gly Asn Val
 515 520 525

Tyr Glu Asp Val Ser Trp Asn Asn Pro Gln Val Phe Ser Cys Leu Thr
 530 535 540

Leu Thr Ala Asp Asp Pro Ala Asn Ile His Ile Thr Asp Leu Ala Ala
 545 550 555 560

Asp Pro Leu Glu Lys Asn Pro Ile His Trp Gly Tyr Gln Gly Asn Trp
 565 570 575

Ala Leu Ser Trp Gln Glu Asp Thr Ala Thr Lys Ser Lys Ala Ala Thr
 580 585 590

Leu Thr Trp Thr Lys Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg Gly
 595 600 605

Thr Leu Val Ala Asn Thr Leu Trp Gly Ser Phe Val Asp Val Arg Ser
 610 615 620

Ile Gln Gln Leu Val Ala Thr Lys Val Arg Gln Ser Gln Glu Thr Arg
 625 630 635 640

Gly Ile Trp Cys Glu Gly Ile Ser Asn Phe Phe His Lys Asp Ser Thr
 645 650 655

Lys Ile Asn Lys Gly Phe Arg His Ile Ser Ala Gly Tyr Val Val Gly
 660 665 670

Ala Thr Thr Thr Leu Ala Ser Asp Asn Leu Ile Thr Ala Ala Phe Cys
 675 680 685

Gln Leu Phe Gly Lys Asp Arg Asp His Phe Ile Asn Lys Asn Arg Ala
 690 695 700

Ser Ala Tyr Ala Ala Ser Leu His Leu Gln His Leu Ala Thr Leu Ser
 705 710 715 720
 Ser Pro Ser Leu Leu Arg Tyr Leu Pro Gly Ser Glu Ser Glu Gln Pro
 725 730 735
 Val Leu Phe Asp Ala Gln Ile Ser Tyr Ile Tyr Ser Lys Asn Thr Met
 740 745 750
 Lys Thr Tyr Thr Gln Ala Pro Lys Gly Glu Ser Ser Trp Tyr Asn
 755 760 765
 Asp Gly Cys Ala Leu Glu Leu Ala Ser Ser Leu Pro His Thr Ala Leu
 770 775 780
 Ser His Glu Gly Leu Phe His Ala Tyr Phe Pro Phe Ile Lys Val Glu
 785 790 795 800
 Ala Ser Tyr Ile His Gln Asp Ser Phe Lys Glu Arg Asn Thr Thr Leu
 805 810 815
 Val Arg Ser Phe Asp Ser Gly Asp Leu Ile Asn Val Ser Val Pro Ile
 820 825 830
 Gly Ile Thr Phe Glu Arg Phe Ser Arg Asn Glu Arg Ala Ser Tyr Glu
 835 840 845
 Ala Thr Val Ile Tyr Val Ala Asp Val Tyr Arg Lys Asn Pro Asp Cys
 850 855 860
 Thr Thr Ala Leu Leu Ile Asn Asn Thr Ser Trp Lys Thr Thr Gly Thr
 865 870 875 880
 Asn Leu Ser Arg Gln Ala Gly Ile Gly Arg Ala Gly Ile Phe Tyr Ala
 885 890 895
 Phe Ser Pro Asn Leu Glu Val Thr Ser Asn Leu Ser Met Glu Ile Arg
 900 905 910
 Gly Ser Ser Arg Ser Tyr Asn Ala Asp Leu Gly Gly Lys Phe Gln Phe
 915 920 925

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGAAAATAC	CCTTGCACAA	ACTCCTGATC	TCTTCGACTC	TTGTCACTCC	CATTCTATTG	60
AGCATTGCAA	CTTACGGAGC	AGATGCTTCT	TTATCCCCTA	CAGATAGCTT	TGATGGAGCG	120
GGCGGCTCTA	CATTTACTCC	AAAATCTACA	GCAGATGCCA	ATGGAACGAA	CTATGTCTTA	180
TCAGGAAATG	TCTATATAAA	CGATGCTGGG	AAAGGCACAG	CATTAACAGG	CTGCTGCTTT	240
ACAGAAACTA	CGGGTGATCT	GACATTACT	GGAAAGGGAT	ACTCATTTTC	ATTCAACACG	300

GTAGATGCGG	GTTCGAATGC	AGGAGCTGCG	GCAAGCACAA	CTGCTGATAA	AGCCCTAACAA	360
TTCACAGGAT	TTTCTAACCT	TTCCCTCATT	GCAGCTCCTG	GAACTACAGT	TGCTTCAGGA	420
AAAAGTACTT	TAAGTTCTGC	AGGAGCCTTA	AATCTTACCG	ATAATGGAAC	GATTCTCTTT	480
AGCCAAAACG	TCTCCAATGA	AGCTAATAAC	AATGGCGGAG	CGATCACCCAC	AAAAACTCTT	540
TCTATTCTG	GGAATACCTC	TTCTATAACC	TTCACTAGTA	ATAGCGCAA	AAAATTAGGT	600
GGAGCGATCT	ATAGCTCTGC	GGCTGCAAGT	ATTTCAGGAA	ACACCGGCCA	GTTAGTCTTT	660
ATGAATAATA	AAGGAGAAC	TGGGGGCGGG	GCTCTGGCT	TTGAAGCCAG	CTCCTCGATT	720
ACTCAAAATA	GCTCCCTTTT	CTTCTCTGGA	AAACACTGCA	CAGATGCTGC	AGGCAAGGGC	780
GGGGCCATT	ATTGTGAAA	AACAGGAGAG	ACTCCTACTC	TTACTATCTC	TGGAAATAAA	840
AGTCTGACCT	TCGCCGAGAA	CTCTTCAGTA	ACTCAAGGCG	GAGCAATCTG	TGCCCATGGT	900
CTAGATCTT	CCGCTGCTGG	CCCTACCCCA	TTTCAAAATA	ATAGATGCGG	GAACACAGCT	960
GCAGGCAAGG	GCGCGCTAT	TGCAATTGCC	GACTCTGGAT	CTTAAAGTCT	CTCTGCAAAT	1020
CAAGGAGACA	TCACGTTCT	TGGCAACACT	CTAACCTCAA	CCTCCGCGCC	AACATCGACA	1080
CGGAATGCTA	TCTACCTGGG	ATCGTCAGCA	AAAATTACGA	ACTTAAGGGC	AGCCCAAGGC	1140
CAATCTATCT	ATTCTATGA	TCCGATTGCA	TCTAACACCA	CAGGAGCTTC	AGACGTTCTG	1200
ACCATCAACC	AACCGGATAG	CAACTCGCCT	TTAGATTATT	CAGGAACGAT	TGTATTTCT	1260
GGGGAAAAGC	TCTCTGCAGA	TGAAGCGAAA	GCTGCTGATA	ACTTCACATC	TATATTAAG	1320
CAACCATTGG	CTCTAGCCTC	TGGAACCTTA	GCACTCAAAG	GAAATGTCGA	GTTAGATGTC	1380
AATGGTTCA	CACAGACTGA	AGGCTCTACA	CTCCTCATGC	AACCAGGAAC	AAAGCTCAA	1440
GCAGATACTG	AACTATCAG	TCTTACAAA	CTTGTGTTG	ATCTTCTGC	CTTAGAGGGA	1500
AATAAGAGT	TGTCCATTGA	AACAGCAGGA	GCCAACAAAA	CTATAACTCT	AACCTCTCCT	1560
CTTGTTCCTC	AAGATAGTAG	CGGCAATT	TATGAAAGCC	ATACGATAAA	CCAAGCCTTC	1620
ACGCAGCCTT	TGGTGGTATT	CACTGCTGCT	ACTGCTGCTA	GCGATATTAA	TATCGATGCG	1680
CTTCTCACTT	CTCCAGTACA	AACTCCAGAA	CCTCATTACG	GGTATCAGGG	ACATTGGGAA	1740
GCCACTTGGG	CAGACACATC	AACTGCAAA	TCAGGAACTA	TGACTTGGGT	AACTACGGGC	1800
TACAACCCCA	ATCCTGAGCG	TAGAGCTTCC	GTAGTTCCCG	ATTCTATTATG	GGCATCCTTT	1860
ACTGACATT	GCACTCTACA	GCAGATCATG	ACATCTCAAG	CGAATAGTAT	CTATCAGCAA	1920
CGAGGACTCT	GGGCATCAGG	AACTGCGAAT	TTCTTCCATA	AGGATAAAATC	AGGAACAAAC	1980
CAAGCATTCC	GACATAAAAG	CTACGGCTAT	ATTGTTGGAG	GAAGTGTGTA	AGATTTTCT	2040
GAAAATATCT	TCAGTGTAGC	TTTCTGCCAG	CTCTCGGTA	AAGATAAAAGA	CCTGTTATA	2100
GTTGAAAATA	CCTCTCATAA	CTATTAGCG	TCGCTATACC	TGCAACATCG	AGCATCCCTA	2160
GGAGGACTTC	CCATGCCCTC	ATTGGAAGT	ATCACCGACA	TGCTGAAAGA	TATTCTCTC	2220
ATTTTGATG	CCCAGCTAAG	CTACAGCTAC	ACTAAAAATG	ATATGGATAC	TCGCTATACT	2280
TCCTATCCTG	AAGCTCAAGG	TTCTTGGACC	AATAATTCTG	GGGCTCTAGA	GCTCGGAGGA	2340
TCTCTGGCTC	TATATCTCCC	TAAGAAGCA	CCGTTCTCC	AGGGATATT	CCCCTTCTTA	2400
AAGTCCAGG	CAGTCTACAG	CCGCCAACAA	AACTTTAAAG	AGAGTGGCGC	TGAAGCCCGT	2460
GCTTTGATG	ATGGAGACCT	AGTGAACCTG	TCTATCCCTG	TCGGCATTG	GTTAGAAAAAA	2520
ATCTCCGAAG	ATGAAAAAAA	TAATTTCGAG	ATTCTCTAG	CCAACATTGG	TGATGTGTAT	2580
CGTAAAAATC	CCCGTTCGCG	TACTTCTCTA	ATGGTCAGT	GAGCCTCTTG	GACTTCGCTA	2640
TGTAAAAACC	TCGCACGACA	AGCCTCTTA	GCAAGTGTG	GAAGCCATCT	GACTCTCTCC	2700
CCTCATGTAG	AACTCTCTGG	GGAAAGCTGCT	TATGAGCTTC	GTGGCTCAGC	ACACATCTAC	2760
AATGTAGATT	GTGGGCTAAG	ATACTCATTC	TAG			2793

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 930 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Lys Ile Pro Leu His Lys Leu Leu Ile Ser Ser Thr Leu Val Thr
1 5 10 15

Pro Ile Leu Leu Ser Ile Ala Thr Tyr Gly Ala Asp Ala Ser Leu Ser
 20 25 30

 Pro Thr Asp Ser Phe Asp Gly Ala Gly Gly Ser Thr Phe Thr Pro Lys
 35 40 45

 Ser Thr Ala Asp Ala Asn Gly Thr Asn Tyr Val Leu Ser Gly Asn Val
 50 55 60
 Tyr Ile Asn Asp Ala Gly Lys Gly Thr Ala Leu Thr Gly Cys Cys Phe
 65 70 75 80

 Thr Glu Thr Thr Gly Asp Leu Thr Phe Thr Gly Lys Gly Tyr Ser Phe
 85 90 95

 Ser Phe Asn Thr Val Asp Ala Gly Ser Asn Ala Gly Ala Ala Ser
 100 105 110

 Thr Thr Ala Asp Lys Ala Leu Thr Phe Thr Gly Phe Ser Asn Leu Ser
 115 120 125

 Phe Ile Ala Ala Pro Gly Thr Thr Val Ala Ser Gly Lys Ser Thr Leu
 130 135 140

 Ser Ser Ala Gly Ala Leu Asn Leu Thr Asp Asn Gly Thr Ile Leu Phe
 145 150 155 160

 Ser Gln Asn Val Ser Asn Glu Ala Asn Asn Asn Gly Gly Ala Ile Thr
 165 170 175

 Thr Lys Thr Leu Ser Ile Ser Gly Asn Thr Ser Ser Ile Thr Phe Thr
 180 185 190

 Ser Asn Ser Ala Lys Lys Leu Gly Gly Ala Ile Tyr Ser Ser Ala Ala
 195 200 205

 Ala Ser Ile Ser Gly Asn Thr Gly Gln Leu Val Phe Met Asn Asn Lys
 210 215 220

 Gly Glu Thr Gly Gly Ala Leu Gly Phe Glu Ala Ser Ser Ser Ile
 225 230 235 240

 Thr Gln Asn Ser Ser Leu Phe Phe Ser Gly Asn Thr Ala Thr Asp Ala
 245 250 255

 Ala Gly Lys Gly Gly Ala Ile Tyr Cys Glu Lys Thr Gly Glu Thr Pro
 260 265 270

 Thr Leu Thr Ile Ser Gly Asn Lys Ser Leu Thr Phe Ala Glu Asn Ser
 275 280 285

 Ser Val Thr Gln Gly Gly Ala Ile Cys Ala His Gly Leu Asp Leu Ser
 290 295 300

 Ala Ala Gly Pro Thr Leu Phe Ser Asn Asn Arg Cys Gly Asn Thr Ala
 305 310 315 320

 Ala Gly Lys Gly Gly Ala Ile Ala Ile Ala Asp Ser Gly Ser Leu Ser
 325 330 335

Leu Ser Ala Asn Gln Gly Asp Ile Thr Phe Leu Gly Asn Thr Leu Thr
 340 345 350

Ser Thr Ser Ala Pro Thr Ser Thr Arg Asn Ala Ile Tyr Leu Gly Ser
 355 360 365

Ser Ala Lys Ile Thr Asn Leu Arg Ala Ala Gln Gly Gln Ser Ile Tyr
 370 375 380

Phe Tyr Asp Pro Ile Ala Ser Asn Thr Thr Gly Ala Ser Asp Val Leu
 385 390 395 400

Thr Ile Asn Gln Pro Asp Ser Asn Ser Pro Leu Asp Tyr Ser Gly Thr
 405 410 415

Ile Val Phe Ser Gly Glu Lys Leu Ser Ala Asp Glu Ala Lys Ala Ala
 420 425 430

Asp Asn Phe Thr Ser Ile Leu Lys Gln Pro Leu Ala Leu Ala Ser Gly
 435 440 445

Thr Leu Ala Leu Lys Gly Asn Val Glu Leu Asp Val Asn Gly Phe Thr
 450 455 460

Gln Thr Glu Gly Ser Thr Leu Leu Met Gln Pro Gly Thr Lys Leu Lys
 465 470 475 480

Ala Asp Thr Glu Ala Ile Ser Leu Thr Lys Leu Val Val Asp Leu Ser
 485 490 495

Ala Leu Glu Gly Asn Lys Ser Val Ser Ile Glu Thr Ala Gly Ala Asn
 500 505 510

Lys Thr Ile Thr Leu Thr Ser Pro Leu Val Phe Gln Asp Ser Ser Gly
 515 520 525

Asn Phe Tyr Glu Ser His Thr Ile Asn Gln Ala Phe Thr Gln Pro Leu
 530 535 540

Val Val Phe Thr Ala Ala Thr Ala Ala Ser Asp Ile Tyr Ile Asp Ala
 545 550 555 560

Leu Leu Thr Ser Pro Val Gln Thr Pro Glu Pro His Tyr Gly Tyr Gln
 565 570 575

Gly His Trp Glu Ala Thr Trp Ala Asp Thr Ser Thr Ala Lys Ser Gly
 580 585 590

Thr Met Thr Trp Val Thr Thr Gly Tyr Asn Pro Asn Pro Glu Arg Arg
 595 600 605

Ala Ser Val Val Pro Asp Ser Leu Trp Ala Ser Phe Thr Asp Ile Arg
 610 615 620

Thr Leu Gln Gln Ile Met Thr Ser Gln Ala Asn Ser Ile Tyr Gln Gln
 625 630 635 640

Arg Gly Leu Trp Ala Ser Gly Thr Ala Asn Phe Phe His Lys Asp Lys
 645 650 655

Ser Gly Thr Asn Gln Ala Phe Arg His Lys Ser Tyr Gly Tyr Ile Val
 660 665 670

Gly Gly Ser Ala Glu Asp Phe Ser Glu Asn Ile Phe Ser Val Ala Phe
 675 680 685

Cys Gln Leu Phe Gly Lys Asp Lys Asp Leu Phe Ile Val Glu Asn Thr
 690 695 700

Ser His Asn Tyr Leu Ala Ser Leu Tyr Leu Gln His Arg Ala Phe Leu
 705 710 715 720

Gly Gly Leu Pro Met Pro Ser Phe Gly Ser Ile Thr Asp Met Leu Lys
 725 730 735

Asp Ile Pro Leu Ile Leu Asn Ala Gln Leu Ser Tyr Ser Tyr Thr Lys
 740 745 750

Asn Asp Met Asp Thr Arg Tyr Thr Ser Tyr Pro Glu Ala Gln Gly Ser
 755 760 765

Trp Thr Asn Asn Ser Gly Ala Leu Glu Leu Gly Gly Ser Leu Ala Leu
 770 775 780

Tyr Leu Pro Lys Glu Ala Pro Phe Phe Gln Gly Tyr Phe Pro Phe Leu
 785 790 795 800

Lys Phe Gln Ala Val Tyr Ser Arg Gln Gln Asn Phe Lys Glu Ser Gly
 805 810 815

Ala Glu Ala Arg Ala Phe Asp Asp Gly Asp Leu Val Asn Cys Ser Ile
 820 825 830

Pro Val Gly Ile Arg Leu Glu Lys Ile Ser Glu Asp Glu Lys Asn Asn
 835 840 845

Phe Glu Ile Ser Leu Ala Asn Ile Gly Asp Val Tyr Arg Lys Asn Pro
 850 855 860

Arg Ser Arg Thr Ser Leu Met Val Ser Gly Ala Ser Trp Thr Ser Leu
 865 870 875 880

Cys Lys Asn Leu Ala Arg Gln Ala Phe Leu Ala Ser Ala Gly Ser His
 885 890 895

Leu Thr Leu Ser Pro His Val Glu Leu Ser Gly Glu Ala Ala Tyr Glu
 900 905 910

Leu Arg Gly Ser Ala His Ile Tyr Asn Val Asp Cys Gly Leu Arg Tyr
 915 920 925

Ser Phe
 930

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 840 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAAGACAATA	TAAGGTACCG	TCATAACAGC	GGGGGTTATG	CACTAGGGAT	CACAGCAACA	60
ACTCCTGCCG	AGGATCAGCT	TACTTTGCC	TTCTGCCAGC	TCTTGCTAG	AGATCGCAAT	120
CATATTACAG	GTAAGAACCA	CGGAGATACT	TACGGGTGCCT	CTTTGTATTT	CCACCATAACA	180
GAAGGGCTCT	TCGACATCGC	CAATTCCCTC	TGGGGAAAAG	CAACCCGAGC	TCCCTGGGTG	240
CTCTCTGAGA	TCTCCAGAT	CATTCCCTTA	TCGTTGATG	CTAAATTCAAG	TTATCTCCAT	300
ACAGACAACC	ACATGAAGAC	ATATTATACC	GATAACTCTA	TCATCAAGGG	TTCTTGGAGA	360
AACGATGCCT	TCTGTGCAGA	TCTTGGAGCT	AGCCTGCCTT	TTGTTATTTC	CGTTCCGTAT	420
CTTCTGAAAG	AAGTCGAACCC	TTTTGTCAAA	GTACAGTATA	TCTATGCGCA	TCAGCAAGAC	480
TTCTACGAGC	GTCATGCTGA	AGGACCGCGCT	TTCAATAAAA	GCGAGCTTAT	CAACGTAGAG	540
ATTCCTATAG	GCGTCACCTT	CGAAAGAGAC	TCAAAATCAG	AAAAGGGAAC	TTACGATCTT	600
ACTCTTATGT	ATATACTCGA	TGCTTACCGA	CGCAATCCTA	AATGTCAAAC	TTCCCTAATA	660
GCTAGCGATG	CTAACTGGAT	GGCCTATGGT	ACCAACCTCG	CACGACAAGG	TTTTCTGT	720
CGTGCTGCGA	ACCATTCCA	AGTGAACCCC	CACATGGAAA	TCTTCGGTCA	ATTGCTTTT	780
GAAGTACGAA	GTTCTCACG	AAATTATAAT	ACAAACCTAG	GCTCTAAAGTT	TTGTTCTAG	840

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Glu	Asp	Asn	Ile	Arg	Tyr	Arg	His	Asn	Ser	Gly	Gly	Tyr	Ala	Lle	Gly
1				5				10					15		
Ile	Thr	Ala	Thr	Thr	Pro	Ala	Glu	Asp	Gln	Lle	Thr	Phe	Ala	Phe	Cys
				20				25				30			
Gln	Lle	Phe	Ala	Arg	Asp	Arg	Asn	His	Ile	Thr	Gly	Lys	Asn	His	Gly
	35						40				45				
Asp	Thr	Tyr	Gly	Ala	Ser	Lle	Tyr	Phe	His	His	Thr	Glu	Gly	Lle	Phe
		50				55			60						
Asp	Ile	Ala	Asn	Phe	Lle	Trp	Gly	Lys	Ala	Thr	Arg	Ala	Pro	Trp	Val
	65				70			75					80		
Lle	Ser	Glu	Ile	Ser	Gln	Ile	Ile	Pro	Lle	Ser	Phe	Asp	Ala	Lys	Phe
		85						90				95			
Ser	Tyr	Lle	His	Thr	Asp	Asn	His	Met	Lys	Thr	Tyr	Tyr	Thr	Asp	Asn
		100						105				110			

Ser Ile Ile Lys Gly Ser Trp Arg Asn Asp Ala Phe Cys Ala Asp Leu
 115 120 125

Gly Ala Ser Leu Pro Phe Val Ile Ser Val Pro Tyr Leu Leu Lys Glu
 130 135 140

Val Glu Pro Phe Val Lys Val Gln Tyr Ile Tyr Ala His Gln Gln Asp
 145 150 155 160

Phe Tyr Glu Arg His Ala Glu Gly Arg Ala Phe Asn Lys Ser Glu Leu
 165 170 175

Ile Asn Val Glu Ile Pro Ile Gly Val Thr Phe Glu Arg Asp Ser Lys
 180 185 190

Ser Glu Lys Gly Thr Tyr Asp Leu Thr Leu Met Tyr Ile Leu Asp Ala
 195 200 205

Tyr Arg Arg Asn Pro Lys Cys Gln Thr Ser Leu Ile Ala Ser Asp Ala
 210 215 220

Asn Trp Met Ala Tyr Gly Thr Asn Leu Ala Arg Gln Gly Phe Ser Val
 225 230 235 240

Arg Ala Ala Asn His Phe Gln Val Asn Pro His Met Glu Ile Phe Gly
 245 250 255

Gln Phe Ala Phe Glu Val Arg Ser Ser Ser Arg Asn Tyr Asn Thr Asn
 260 265 270

Leu Gly Ser Lys Phe Cys Phe
 275

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1545 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGACCATAAC	TTCGAAATTTC	TCTTACCTGC	TCGGCTTTAT	TCCTCGCTCT	CCCTGCAGCA	60
GCACAAGTTG	TATATCTTCA	TGAAAGTGAT	GGTTATAACG	GTGCTATCAA	TAATAAAAGC	120
TTAGAACCTA	AAATTACCTG	TTATCCAGAA	GGAACCTTCTT	ACATCTTCT	AGATGACGTG	180
AGGATTTCGA	ACGTTAAGCA	TGATCAAGAA	GATGCTGGGG	TTTTTATAAA	TCGATCTGGG	240
AATCTTTTTT	TCATGGCAA	CCGTTGCAAC	TTCACCTTTTC	ACAACCTTAT	GACCGAGGGT	300
TTTGGCGCTG	CCATTTCGAA	CCGCGTTGGA	GACACCACTC	TCACTCTCTC	TAATTTTCT	360
TACTTAACGT	TCACCTCAGC	ACCTCTACTA	CCTCAAGGAC	AAGGAGCGAT	TTATAGTCTT	420
GGTTCCGTGA	TGATCGAAA	TAGTGAGGAA	GTGACTTTCT	GTGGGAACTA	CTCTTCGTGG	480
AGTGGAGCTG	CGATTATAC	TCCCTACCTT	TTAGGTTCTA	AGGCGAGTCG	TCCTTCAGTA	540
AATCTCAGCG	GGAAACCGCTA	CCTGGTGTTT	AGAGACTATG	TGAGCCAAGG	TTATGGCGGC	600
GCCGTATCTA	CCCACAATCT	CACACTCACG	ACTCGAGGAC	CTTCGTGTTT	TGAAAATAAT	660
CATGCTTATC	ATGACGTGAA	TAGTAATGGA	GGAGCCATTG	CCATTGCTCC	TGGAGGATCG	720

ATCTCTATAT	CCGTGAAAAG	CGGAGATCTC	ATCTTCAAAG	GAAATACAGC	ATCACAAGAC	780
GGAAATACAA	TACACAACTC	CATCCATCTG	CAATCTGGAG	CACAGTTAA	GAACCTACGT	840
GCTGTTCAAG	AATCCGGAGT	TTATTTCTAT	GATCCTATAA	GCCATAGCGA	GTCGCATAAA	900
ATTACAGATC	TTGTAATCAA	TGCTCCTGAA	GGAAAGGAAA	CTTATGAAGG	AACAATTAGC	960
TTCTCAGGAC	TATGCTCTGGA	TGATCATGAA	GTTCGTGCGG	AAAATCTTAC	TTCCACAATC	1020
CTACAAGATG	TCACATTAGC	AGGAGGAACT	CTCTCTCTAT	CGGATGGGGT	TACCTTGCAA	1080
CTGCATTCTT	TTAACAGAGGA	AGCAAGCTCT	ACGCCCTACTA	TGTCTCCAGG	AACCACCTTG	1140
CTCTGCTCA	GAGATGCTCG	GGTTCAAGAAT	CTGCACATCC	TGATTGAAGA	TACCGACAAC	1200
TTTGTTCCTG	TAAGGATTGCG	CGCCGAGGAGC	AAGGATGCTC	TTGTCTCATT	AGAAAAAAACTT	1260
AAAGTTGCCT	TTGAGGCTTA	TTGGTCCGTC	TATGACTTTC	CTCAATTAA	GGAAGCCTTT	1320
ACGATTCCCTC	TTCTTGAAC	TCTAGGGCCT	TCTTTGACA	GTCTTCTCCT	AGGGGAGACC	1380
ACTTGGAGA	GAACCCAAGT	CACAACAGAG	AATGACGCCG	TTCGAGGTTT	CTGGTCCCTA	1440
AGCTGGGAAG	AGTACCCCCC	TTCTCTGGAT	AAAGACAGAA	GGATCACACC	AACTAAGAAA	1500
ACTGTTTCC	TCACTTGGAA	TCCTGAGATC	ACTTCTACGC	CATAA		1545

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 514 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Thr	Ile	Leu	Arg	Asn	Phe	Leu	Thr	Cys	Ser	Ala	Leu	Phe	Leu	Ala
1						5				10					15
Leu	Pro	Ala	Ala	Ala	Gln	Val	Val	Tyr	Leu	His	Glu	Ser	Asp	Gly	Tyr
						20			25					30	
Asn	Gly	Ala	Ile	Asn	Asn	Lys	Ser	Leu	Glu	Pro	Lys	Ile	Thr	Cys	Tyr
						35			40				45		
Pro	Glu	Gly	Thr	Ser	Tyr	Ile	Phe	Leu	Asp	Asp	Val	Arg	Ile	Ser	Asn
						50			55				60		
Val	Lys	His	Asp	Gln	Glu	Asp	Ala	Gly	Val	Phe	Ile	Asn	Arg	Ser	Gly
						65			70				75		80
Asn	Leu	Phe	Phe	Met	Gly	Asn	Arg	Cys	Asn	Phe	Thr	Phe	His	Asn	Leu
						85			90				95		
Met	Thr	Glu	Gly	Phe	Gly	Ala	Ala	Ile	Ser	Asn	Arg	Val	Gly	Asp	Thr
						100			105				110		
Thr	Leu	Thr	Leu	Ser	Asn	Phe	Ser	Tyr	Leu	Thr	Phe	Thr	Ser	Ala	Pro
						115			120				125		
Leu	Leu	Pro	Gln	Gly	Gln	Gly	Ala	Ile	Tyr	Ser	Leu	Gly	Ser	Val	Met
						130			135				140		
Ile	Glu	Asn	Ser	Glu	Glu	Val	Thr	Phe	Cys	Gly	Asn	Tyr	Ser	Ser	Trp
						145			150				155		160
Ser	Gly	Ala	Ala	Ile	Tyr	Thr	Pro	Tyr	Leu	Leu	Gly	Ser	Lys	Ala	Ser

165	170	175
Arg Pro Ser Val Asn Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp		
180	185	190
Tyr Val Ser Gln Gly Tyr Gly Ala Val Ser Thr His Asn Leu Thr		
195	200	205
Leu Thr Thr Arg Gly Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His		
210	215	220
Asp Val Asn Ser Asn Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser		
225	230	235
		240
Ile Ser Ile Ser Val Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr		
245	250	255
Ala Ser Gln Asp Gly Asn Thr Ile His Asn Ser Ile His Leu Gln Ser		
260	265	270
Gly Ala Gln Phe Lys Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr		
275	280	285
Phe Tyr Asp Pro Ile Ser His Ser Glu Ser His Lys Ile Thr Asp Leu		
290	295	300
Val Ile Asn Ala Pro Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser		
305	310	315
		320
Phe Ser Gly Leu Cys Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu		
325	330	335
Thr Ser Thr Ile Leu Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser		
340	345	350
Leu Ser Asp Gly Val Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala		
355	360	365
Ser Ser Thr Leu Thr Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly		
370	375	380
Asp Ala Arg Val Gln Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn		
385	390	395
		400
Phe Val Pro Val Arg Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser		
405	410	415
Leu Glu Lys Leu Lys Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp		
420	425	430
Phe Pro Gln Phe Lys Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu		
435	440	445
Gly Pro Ser Phe Asp Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg		
450	455	460
Thr Gln Val Thr Thr Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu		
465	470	475
		480

Ser Trp Glu Glu Tyr Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr
 485 490 495

Pro Thr Lys Lys Thr Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser
 500 505 510

Thr Pro

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 787 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAAAACGT	CTATTCTGAA	GTTCTTAATT	TCTACCACAC	TGGCGCCATG	TTTGCTTCA	60
ACAGCGTTA	CTGTAGAAGT	TATCATGCCT	TCCGAGAACT	TTGATGGATC	GAGTGGGAAG	120
ATTTTCCTT	ACACAAACACT	TTCTGATCCT	AGAGGGACAC	TCTGTATTTT	TTCAAGGGAT	180
CTCTACATTG	CGAACATTGAA	TAATGCCATA	TCCAGAACCT	CTTCCAGTTG	CTTAGCAAT	240
AGGGCGGGAG	CACTACAAAT	CTTAGGAAAA	GGTGGGGTTT	TCTCCTCTT	AAATATCCGT	300
TCTTCAGCTG	ACGGAGCCGC	GATTAGTAGT	GTAATCACCC	AAAATCCTGA	ACTATGTCCC	360
TTGAGTTTTT	CAGGATTAG	TCAGATGATC	TTCGATAACT	GTGAATCTT	GACTTCAGAT	420
ACCTCAGCGA	GTAATGTCAT	ACCTCACGCA	TCGGCGATTT	ACGCTACAAC	GCCCATGCTC	480
TTTACAAACA	ATGACTCCAT	ACTATTCCAA	TACAACCGTT	CTGCAGGATT	TGGAGCTGCC	540
ATTCGAGGCA	CAAGCATCAC	AATAGAAAAAT	ACGAAAAAAGA	GCCTTCTCTT	TAATGGTAAT	600
GGATCCATCT	CTAATGGAGG	GGCCCTCACG	GGATCTGCAG	CGATCAACCT	CATCAACAAAT	660
AGCGCTCCTG	TGATTCTCTC	AACGAATGCT	ACAGGGATCT	ATGGTGGGC	TATTTACCTT	720
ACCGGAGGAT	CTATGCTCAC	CTCTGGGAAC	CTCTCAGGAG	TCTTGTTCGT	TTATAATAGC	780
TCGCGCT						787

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Lys Thr Ser Ile Arg Lys Phe Leu Ile Ser Thr Thr Leu Ala Pro
 1 5 10 15

Cys Phe Ala Ser Thr Ala Phe Thr Val Glu Val Ile Met Pro Ser Glu
 20 25 30

Asn Phe Asp Gly Ser Ser Gly Lys Ile Phe Pro Tyr Thr Thr Leu Ser
 35 40 45

Asp Pro Arg Gly Thr Leu Cys Ile Phe Ser Gly Asp Leu Tyr Ile Ala
 50 55 60

Asn Leu Asp Asn Ala Ile Ser Arg Thr Ser Ser Ser Cys Phe Ser Asn
 65 70 75 80

Arg Ala Gly Ala Leu Gln Ile Leu Gly Lys Gly Gly Val Phe Ser Phe
 85 90 95

Leu Asn Ile Arg Ser Ser Ala Asp Gly Ala Ala Ile Ser Ser Val Ile
 100 105 110

Thr Gln Asn Pro Glu Leu Cys Pro Leu Ser Phe Ser Gly Phe Ser Gln
 115 120 125

Met Ile Phe Asp Asn Cys Glu Ser Leu Thr Ser Asp Thr Ser Ala Ser
 130 135 140

Asn Val Ile Pro His Ala Ser Ala Ile Tyr Ala Thr Thr Pro Met Leu
 145 150 155 160

Phe Thr Asn Asn Asp Ser Ile Leu Phe Gln Tyr Asn Arg Ser Ala Gly
 165 170 175

Phe Gly Ala Ala Ile Arg Gly Thr Ser Ile Thr Ile Glu Asn Thr Lys
 180 185 190

Lys Ser Leu Leu Phe Asn Gly Asn Gly Ser Ile Ser Asn Gly Gly Ala
 195 200 205

Leu Thr Gly Ser Ala Ala Ile Asn Leu Ile Asn Asn Ser Ala Pro Val
 210 215 220

Ile Phe Ser Thr Asn Ala Thr Gly Ile Tyr Gly Gly Ala Ile Tyr Leu
 225 230 235 240

Thr Gly Gly Ser Met Leu Thr Ser Gly Asn Leu Ser Gly Val Leu Phe
 245 250 255

Val Tyr Asn Ser Ser Arg
 260

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2838 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGAAGACTT CAGTTCTAT GTTGTTGGCC CTGCTTTGCT CGGGGGCTAG CTCTATTGTA	60
CTCCATGCCG CAACCACTCC ACTAAATCCT GAAGATGGGT TTATTGGGA GGGCAATACA	120
AATACTTTT CTCCGAAATC TACAACGGAT GCTGCAGGAA CTACCTACTC TCTCACAGGA	180
GAGGTTCTGT TTATAGATCC GGGGAAAGGT GGTTCAATT A CAGGAACTTG CTTTGTAGAA	240

ACTGCTGGCG	ATCTTACATT	TTTAGGTAAT	GGAAATACCC	TAAAGTCCT	GTCGGTAGAT	300
GCAGGTGCTA	ATATCGCGGT	TGCTCATGTA	CAAGGAAGTA	AGAATTAAAG	CTTCACAGAT	360
TTCCTTCCTC	TGGTGATCAC	AGAATCTCCA	AAATCCGCTG	TTAGTACAGG	AAAAGGTAGC	420
CTAGTCAGTT	CAGGTGCAGT	CCAACTGCAA	GATATAAACAA	CTCTAGTTCT	TACAAGCAAT	480
GCCTCTGTCG	AAGATGGTGG	CGTGATTAAA	GGAAACTCCT	GCTTGATTCA	GGGAATCAA	540
AATAGTGCGA	TTTTGGACA	AAATACATCT	TCGAAAAAAG	GAGGGCGAT	CTCCACGACT	600
CAAGGACTCA	CCATAGAGAA	TAACCTAGGG	ACGCTAAAGT	TCAATGAAAAA	CAAAGCAGTG	660
ACCTCAGGAG	GCGCCTTAGA	TTTAGGAGCC	GCGTCTACAT	TCACTGCGAA	CCATGAGTTG	720
ATATTTTCAC	AAAATAAGAC	TTCTGGGAAT	GCTGCAAATG	GCGGAGCCAT	AAATTGCTCA	780
GGCGACCTAA	CATTTACTGA	TAACACTTCT	TTGTTACTTC	AAGAAAATAG	CACAATGCAG	840
GATGGTGGAG	CTTTGTGTAG	CACAGGAACC	ATAAGCATTAA	CCGGTAGTGA	TTCTATCAAT	900
GTGATAGGAA	ATACTTCAGG	ACAAAAAAGGA	GGAGCGATT	CTGCAGCTTC	TCTCAAGATT	960
TTGGGAGGGC	AGGGAGGC	TCTCTTTCT	AATAACGTAG	TGACTCATGC	CACCCCTCTA	1020
GGAGGTGCCA	TTTTTATCAA	CACAGGAGGA	TCCTTGAGC	TCTTCACTCA	AGGAGGGGAT	1080
ATCGTATTG	AGGGAAATCA	GGTCACTACA	ACAGCTCCAA	ATGCTACCAC	TAAGAGAAAAT	1140
GTAATTCA	TCGAGAGCAC	CGCGAAGTGG	ACGGGACTTG	CTGCAAGTCA	AGGTAACGCT	1200
ATCTATTCCT	ATGATCCC	TACCACCAAC	GATACGGGAG	CAAGCGATAA	CTTACGTATC	1260
AATGAGGTCA	GTGCAAATCA	AAAGCTCTCG	GGATCTATAG	TATTTCTGG	AGAGAGATTG	1320
TCGACAGCAG	AAGCTATAGC	TGAAAATCTT	ACTTCGAGGA	TCAACCAGCC	TGTCACCTT	1380
GTAGAGGGGA	GCTTAGAACT	AAACAGGGGA	GTGACCTTG	TCACACAAAGG	ATTCTCGCAG	1440
GAGCCAGAA	CCACGCTTCT	TTTGGATTG	GGGACCTCAT	TACAAGCTTC	TACAGAAGAT	1500
ATCGTCATCA	CAAATTCA	TATAATGCC	GATACCATT	ACGGAAAGAA	TCCAATCAAT	1560
ATTGTAGCT	CAGCAGCGAA	TAAGAACATT	ACCCCTAACAG	GAACCTTAGC	ACTTGTAAAAT	1620
GCAGATGGAG	CTTTGTATGA	GAACCATACC	TTGCAAGACT	CTCAAGATTA	TAGCTTTGTA	1680
AAGTTATCTC	CAGGAGCGGG	AGGGACTATA	ATTACTCAAG	ATGCTTCCTCA	GAAGCTTCTT	1740
GAAGTAGCTC	CTTCTAGACC	ACATTATGGC	TATCAAGGAC	ATTGGAATGT	GCAAGTCATC	1800
CCAGGAACGG	GAACCTCAACC	GAGCCAGGCA	AATTAGAAT	GGGTGCGGAC	AGGATACCTT	1860
CCGAATCCCG	AACGGCAAGG	ATTTTTAGTT	CCCAATAGCC	TGTGGGTT	TTTGTGTTGAT	1920
CAGCGTGC	TCCAAGAAAT	CATGGTAAAT	AGTAGCCAA	TCTTATGTC	GGAACGGGGA	1980
GTCGGGGAG	CTGGAATTG	TAATTCTCTA	CATAGAGATA	AAATTAATGA	GCACGGCTAT	2040
CGCCATAGCG	GTGTCGGTTA	TCTTGTGGGA	GTTGGCACTC	ATGCTTTTC	TGATGCTACG	2100
ATAAAATGCG	CTTTTGCCA	GCTCTTCAGT	AGAGATAAAAG	ACTACGTAGT	ATCCAAAAAAT	2160
CATGGAACTA	GCTACTCAGG	GGTCGTATT	CTTGAGGATA	CCCTAGAGTT	TAGAAGTCCA	2220
CAGGGATTCT	ATACTGATAG	CTCCTCAGAA	GCTTGCTGTA	ACCAAGTCGT	CACTATAGAT	2280
ATGCAGTTGT	CTTACAGCCA	TAGAAATAAT	GATATGAAAAA	CCAAATACAC	GACATATCCA	2340
GAAGCTCAGG	GATCTGGGC	AAATGATGTT	TTTGGTCTTG	AGTTTGAGC	GACTACATAC	2400
TACTACCTA	ACAGTACTTT	TTTATTGAT	TACTACTCTC	CGTTTCTCAG	GCTGCAGTGC	2460
ACCTATGCTC	ACCAGGAAGA	CTTCAAAGAG	ACAGGAGGTG	AGGTTCGTCA	CTTTACTAGC	2520
GGAGATCTT	TCAATTAGC	AGTTCCCTATT	GGCGTGAAGT	TTGAGAGATT	TTCAGACTGT	2580
AAAAGGGGAT	CTTATGA	ACTCCTGCT	TATGTTCTG	ATGTGATTG	CAAAGATCCC	2640
AAGAGCACGG	CAACATTGGC	TAGTGGAGCT	ACGTGGAGCA	CCCACGGAAA	CAATCTCTCC	2700
AGACAAGGAT	TACAACGTGCG	TTTAGGGAAC	CACTGTCTCA	AAATCCTGG	AATTGAGGTG	2760
TTCAGTCACG	GAGCTATTGA	ATTGCGGGGA	TCCTCTCGTA	ATTATAACAT	CAATCTCGGG	2820
GGTAAATACC	GATTTAA					2838

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 946 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Lys Thr Ser Val Ser Met Leu Leu Ala Leu Leu Cys Ser Gly Ala

1	5	10	15
Ser Ser Ile Val Leu His Ala Ala Thr Thr Pro Leu Asn Pro Glu Asp			
20	25		30
Gly Phe Ile Gly Glu Gly Asn Thr Asn Thr Phe Ser Pro Lys Ser Thr			
35	40		45
Thr Asp Ala Ala Gly Thr Thr Tyr Ser Leu Thr Gly Glu Val Leu Phe			
50	55		60
Ile Asp Pro Gly Lys Gly Ser Ile Thr Gly Thr Cys Phe Val Glu			
65	70		80
Thr Ala Gly Asp Leu Thr Phe Leu Gly Asn Gly Asn Thr Leu Lys Phe			
85	90		95
Leu Ser Val Asp Ala Gly Ala Asn Ile Ala Val Ala His Val Gln Gly			
100	105		110
Ser Lys Asn Leu Ser Phe Thr Asp Phe Leu Ser Leu Val Ile Thr Glu			
115	120		125
Ser Pro Lys Ser Ala Val Ser Thr Gly Lys Gly Ser Leu Val Ser Ser			
130	135		140
Gly Ala Val Gln Leu Gln Asp Ile Asn Thr Leu Val Leu Thr Ser Asn			
145	150		155
160			
Ala Ser Val Glu Asp Gly Gly Val Ile Lys Gly Asn Ser Cys Leu Ile			
165	170		175
Gln Gly Ile Lys Asn Ser Ala Ile Phe Gly Gln Asn Thr Ser Ser Lys			
180	185		190
Lys Gly Gly Ala Ile Ser Thr Thr Gln Gly Leu Thr Ile Glu Asn Asn			
195	200		205
Leu Gly Thr Leu Lys Phe Asn Glu Asn Lys Ala Val Thr Ser Gly Gly			
210	215		220
Ala Leu Asp Leu Gly Ala Ala Ser Thr Phe Thr Ala Asn His Glu Leu			
225	230		240
Ile Phe Ser Gln Asn Lys Thr Ser Gly Asn Ala Ala Asn Gly Gly Ala			
245	250		255
Ile Asn Cys Ser Gly Asp Leu Thr Phe Thr Asp Asn Thr Ser Leu Leu			
260	265		270
Leu Gln Glu Asn Ser Thr Met Gln Asp Gly Gly Ala Leu Cys Ser Thr			
275	280		285
Gly Thr Ile Ser Ile Thr Gly Ser Asp Ser Ile Asn Val Ile Gly Asn			
290	295		300
Thr Ser Gly Gln Lys Gly Gly Ala Ile Ser Ala Ala Ser Leu Lys Ile			
305	310		315
			320

Leu Gly Gly Gln Gly Gly Ala Leu Phe Ser Asn Asn Val Val Thr His
 325 330 335
 Ala Thr Pro Leu Gly Gly Ala Ile Phe Ile Asn Thr Gly Gly Ser Leu
 340 345 350
 Gln Leu Phe Thr Gln Gly Gly Asp Ile Val Phe Glu Gly Asn Gln Val
 355 360 365
 Thr Thr Thr Ala Pro Asn Ala Thr Thr Lys Arg Asn Val Ile His Leu
 370 375 380
 Glu Ser Thr Ala Lys Trp Thr Gly Leu Ala Ala Ser Gln Gly Asn Ala
 385 390 395 400
 Ile Tyr Phe Tyr Asp Pro Ile Thr Thr Asn Asp Thr Gly Ala Ser Asp
 405 410 415
 Asn Leu Arg Ile Asn Glu Val Ser Ala Asn Gln Lys Leu Ser Gly Ser
 420 425 430
 Ile Val Phe Ser Gly Glu Arg Leu Ser Thr Ala Glu Ala Ile Ala Glu
 435 440 445
 Asn Leu Thr Ser Arg Ile Asn Gln Pro Val Thr Leu Val Glu Gly Ser
 450 455 460
 Leu Glu Leu Lys Gln Gly Val Thr Leu Ile Thr Gln Gly Phe Ser Gln
 465 470 475 480
 Glu Pro Glu Ser Thr Leu Leu Leu Asp Leu Gly Thr Ser Leu Gln Ala
 485 490 495
 Ser Thr Glu Asp Ile Val Ile Thr Asn Ser Ser Ile Asn Ala Asp Thr
 500 505 510
 Ile Tyr Gly Lys Asn Pro Ile Asn Ile Val Ala Ser Ala Ala Asn Lys
 515 520 525
 Asn Ile Thr Leu Thr Gly Thr Leu Ala Leu Val Asn Ala Asp Gly Ala
 530 535 540
 Leu Tyr Glu Asn His Thr Leu Gln Asp Ser Gln Asp Tyr Ser Phe Val
 545 550 555 560
 Lys Leu Ser Pro Gly Ala Gly Gly Thr Ile Ile Thr Gln Asp Ala Ser
 565 570 575
 Gln Lys Leu Leu Glu Val Ala Pro Ser Arg Pro His Tyr Gly Tyr Gln
 580 585 590
 Gly His Trp Asn Val Gln Val Ile Pro Gly Thr Gly Thr Gln Pro Ser
 595 600 605
 Gln Ala Asn Leu Glu Trp Val Arg Thr Gly Tyr Leu Pro Asn Pro Glu
 610 615 620

Arg Gln Gly Phe Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Val Asp
 625 630 635 640

Gln Arg Ala Ile Gln Glu Ile Met Val Asn Ser Ser Gln Ile Leu Cys
 645 650 655

Gln Glu Arg Gly Val Trp Gly Ala Gly Ile Ala Asn Phe Leu His Arg
 660 665 670

Asp Lys Ile Asn Glu His Gly Tyr Arg His Ser Gly Val Gly Tyr Leu
 675 680 685

Val Gly Val Gly Thr His Ala Phe Ser Asp Ala Thr Ile Asn Ala Ala
 690 695 700

Phe Cys Gln Leu Phe Ser Arg Asp Lys Asp Tyr Val Val Ser Lys Asn
 705 710 715 720

His Gly Thr Ser Tyr Ser Gly Val Val Phe Leu Glu Asp Thr Leu Glu
 725 730 735

Phe Arg Ser Pro Gln Gly Phe Tyr Thr Asp Ser Ser Ser Glu Ala Cys
 740 745 750

Cys Asn Gln Val Val Thr Ile Asp Met Gln Leu Ser Tyr Ser His Arg
 755 760 765

Asn Asn Asp Met Lys Thr Lys Tyr Thr Tyr Pro Glu Ala Gln Gly
 770 775 780

Ser Trp Ala Asn Asp Val Phe Gly Leu Glu Phe Gly Ala Thr Thr Tyr
 785 790 795 800

Tyr Tyr Pro Asn Ser Thr Phe Leu Phe Asp Tyr Tyr Ser Pro Phe Leu
 805 810 815

Arg Leu Gln Cys Thr Tyr Ala His Gln Glu Asp Phe Lys Glu Thr Gly
 820 825 830

Gly Glu Val Arg His Phe Thr Ser Gly Asp Leu Phe Asn Leu Ala Val
 835 840 845

Pro Ile Gly Val Lys Phe Glu Arg Phe Ser Asp Cys Lys Arg Gly Ser
 850 855 860

Tyr Glu Leu Thr Leu Ala Tyr Val Pro Asp Val Ile Arg Lys Asp Pro
 865 870 875 880

Lys Ser Thr Ala Thr Leu Ala Ser Gly Ala Thr Trp Ser Thr His Gly
 885 890 895

Asn Asn Leu Ser Arg Gln Gly Leu Gln Leu Arg Leu Gly Asn His Cys
 900 905 910

Leu Ile Asn Pro Gly Ile Glu Val Phe Ser His Gly Ala Ile Glu Leu
 915 920 925

Arg Gly Ser Ser Arg Asn Tyr Asn Ile Asn Leu Gly Gly Lys Tyr Arg

930

935

940

Phe
945

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3000 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 259...3000
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATCAGGTGAT AAAAGTCCT CGTTAGCTAG TGACTGTAGG TGACATGAGA AAGCTAACAC	60
GGAGGAAACT AAAACCCAAG GAATCGAACT CTTCATGGTA ATGCTTTGT TTTTAGAGA	120
ACTATTGCA TCAATATAGA AACAAAATAA GTAAATCAAG TTAAAGATGA CAAAACAGCT	180
GTCAGAATT TTTATCTTGA CTCTCTGAGT TTTCTATTTT ATATGACGCA AGTAAGAATT	240
TAATAATAAA GTGGGTTT ATG AAA TCG CAA TTT TCC TGG TTA GTG CTC TCT	291
Met Lys Ser Gln Phe Ser Trp Leu Val Leu Ser	
1 5 10	
TCG ACA TTG GCA TGT TTT ACT AGT TGT TCC ACT GTT TTT GCT GCA ACT	339
Ser Thr Leu Ala Cys Phe Thr Ser Cys Ser Thr Val Phe Ala Ala Thr	
15 20 25	
GCT GAA AAT ATA GGC CCC TCT GAT AGC TTT GAC GGA AGT ACT AAC ACA	387
Ala Glu Asn Ile Gly Pro Ser Asp Ser Phe Asp Gly Ser Thr Asn Thr	
30 35 40	
GGC ACC TAT ACT CCT AAA AAT ACG ACT ACT GGA ATA GAC TAT ACT CTG	435
Gly Thr Tyr Thr Pro Lys Asn Thr Thr Gly Ile Asp Tyr Thr Leu	
45 50 55	
ACA GGA GAT ATA ACT CTG CAA AAC CTT GGG GAT TCG GCA GCT TTA ACG	483
Thr Gly Asp Ile Thr Leu Gln Asn Leu Gly Asp Ser Ala Ala Leu Thr	
60 65 70 75	
AAG GGT TGT TTT TCT GAC ACT ACG GAA TCT TTA AGC TTT GCC GGT AAG	531
Lys Gly Cys Phe Ser Asp Thr Thr Glu Ser Leu Ser Phe Ala Gly Lys	
80 85 90	
GGG TAC TCA CTT TCT TTT TTA AAT ATT AAG TCT AGT GCT GAA GGC GCA	579
Gly Tyr Ser Leu Ser Phe Leu Asn Ile Lys Ser Ser Ala Glu Gly Ala	
95 100 105	
GCA CTT TCT GTT ACA ACT GAT AAA AAT CTG TCG CTA ACA GGA TTT TCG	627

Ala Leu Ser Val Thr Thr Asp Lys Asn Leu Ser Leu Thr Gly Phe Ser			
110	115	120	
AGT CTT ACT TTC TTA GCG GCC CCA TCA TCG GTA ATC ACA ACC CCC TCA			675
Ser Leu Thr Phe Leu Ala Ala Pro Ser Ser Val Ile Thr Thr Pro Ser			
125	130	135	
GGA AAA GGT GCA GTT AAA TGT GGA GGG GAT CTT ACA TTT GAT AAC AAT			723
Gly Lys Gly Ala Val Lys Cys Gly Gly Asp Leu Thr Phe Asp Asn Asn			
140	145	150	155
GGA ACT ATT TTA TTT AAA CAA GAT TAC TGT GAG GAA AAT GGC GGA GCC			771
Gly Thr Ile Leu Phe Lys Gln Asp Tyr Cys Glu Glu Asn Gly Gly Ala			
160	165	170	
ATT TCT ACC AAG AAT CTT TCT TTG AAA AAC AGC ACG GGA TCG ATT TCT			819
Ile Ser Thr Lys Asn Leu Ser Leu Lys Asn Ser Thr Gly Ser Ile Ser			
175	180	185	
TTT GAA GGG AAT AAA TCG AGC GCA ACA GGG AAA AAA GGT GGG GCT ATT			867
Phe Glu Gly Asn Lys Ser Ser Ala Thr Gly Lys Lys Gly Gly Ala Ile			
190	195	200	
TGT GCT ACT GGT ACT GTA GAT ATT ACA AAT AAT ACG GCT CCT ACC CTC			915
Cys Ala Thr Gly Thr Val Asp Ile Thr Asn Asn Thr Ala Pro Thr Leu			
205	210	215	
TTC TCG AAC AAT ATT GCT GAA GCT GCA GGT GGA GCT ATA AAT AGC ACA			963
Phe Ser Asn Asn Ile Ala Glu Ala Ala Gly Gly Ala Ile Asn Ser Thr			
220	225	230	235
GGA AAC TGT ACA ATT ACA GGG AAT ACG TCT CTT GTA TTT TCT GAA AAT			1011
Gly Asn Cys Thr Ile Thr Gly Asn Thr Ser Leu Val Phe Ser Glu Asn			
240	245	250	
AGT GTG ACA GCG ACC GCA GGA AAT GGA GGA GCT CTT TCT GGA GAT GCC			1059
Ser Val Thr Ala Thr Ala Gly Asn Gly Gly Ala Leu Ser Gly Asp Ala			
255	260	265	
GAT GTT ACC ATA TCT GGG AAT CAG AGT GTA ACT TTC TCA GGA AAC CAA			1107
Asp Val Thr Ile Ser Gly Asn Gln Ser Val Thr Phe Ser Gly Asn Gln			
270	275	280	
GCT GTA GCT AAT GGC GGA GCC ATT TAT GCT AAG AAG CTT ACA CTG GCT			1155
Ala Val Ala Asn Gly Gly Ala Ile Tyr Ala Lys Lys Leu Thr Leu Ala			
285	290	295	
TCC GGG GGG GGG GGT ATC TCC TTT TCT AAC AAT ATA GTC CAA GGT			1203
Ser Gly Gly Gly Gly Ile Ser Phe Ser Asn Asn Ile Val Gln Gly			
300	305	310	315
ACC ACT GCA GGT AAT GGT GGA GCC ATT TCT ATA CTG GCA GCT GGA GAG			1251
Thr Thr Ala Gly Asn Gly Gly Ala Ile Ser Ile Leu Ala Ala Gly Glu			
320	325	330	
TGT AGT CTT TCA GCA GAA GCA GGG GAC ATT ACC TTC AAT GGG AAT GCC			1299
Cys Ser Leu Ser Ala Glu Ala Gly Asp Ile Thr Phe Asn Gly Asn Ala			
335	340	345	

ATT GTT GCA ACT ACA CCA CAA ACT ACA AAA AGA AAT TCT ATT GAC ATA Ile Val Ala Thr Thr Pro Gln Thr Thr Lys Arg Asn Ser Ile Asp Ile 350 355 360	1347
GGA TCT ACT GCA AAG ATC ACG AAT TTA CGT GCA ATA TCT GGG CAT AGC Gly Ser Thr Ala Lys Ile Thr Asn Leu Arg Ala Ile Ser Gly His Ser 365 370 375	1395
ATC TTT TTC TAC GAT CCG ATT ACT GCT AAT ACG GCT GCG GAT TCT ACA Ile Phe Phe Tyr Asp Pro Ile Thr Ala Asn Thr Ala Ala Asp Ser Thr 380 385 390 395	1443
GAT ACT TTA AAT CTC AAT AAG GCT GAT GCA GGT AAT AGT ACA GAT TAT Asp Thr Leu Asn Leu Asn Lys Ala Asp Ala Gly Asn Ser Thr Asp Tyr 400 405 410	1491
AGT GGG TCG ATT GTT TTT TCT GGT GAA AAG CTC TCT GAA GAT GAA GCA Ser Gly Ser Ile Val Phe Ser Gly Glu Lys Leu Ser Glu Asp Glu Ala 415 420 425	1539
AAA GTT GCA GAC AAC CTC ACT TCT ACG CTG AAG CAG CCT GTA ACT CTA Lys Val Ala Asp Asn Leu Thr Ser Thr Leu Lys Gln Pro Val Thr Leu 430 435 440	1587
ACT GCA GGA AAT TTA GTA CTT AAA CGT GGT GTC ACT CTC GAT ACG AAA Thr Ala Gly Asn Leu Val Leu Lys Arg Gly Val Thr Leu Asp Thr Lys 445 450 455	1635
GGC TTT ACT CAG ACC GCG GGT TCC TCT GTT ATT ATG GAT GCG GGC ACA Gly Phe Thr Gln Thr Ala Gly Ser Ser Val Ile Met Asp Ala Gly Thr 460 465 470 475	1683
ACG TTA AAA GCA AGT ACA GAG GAG GTC ACT TTA ACA GGT CTT TCC ATT Thr Leu Lys Ala Ser Thr Glu Glu Val Thr Leu Thr Gly Leu Ser Ile 480 485 490	1731
CCT GTA GAC TCT TTA GGC GAG GGT AAG AAA GTT GTA ATT GCT GCT TCT Pro Val Asp Ser Leu Gly Glu Gly Lys Lys Val Val Ile Ala Ala Ser 495 500 505	1779
GCA GCA AGT AAA AAT GTA GCC CTT AGT GGT CCG ATT CTT CTT TTG GAT Ala Ala Ser Lys Asn Val Ala Leu Ser Gly Pro Ile Leu Leu Leu Asp 510 515 520	1827
AAC CAA GGG AAT GCT TAT GAA AAT CAC GAC TTA GGA AAA ACT CAA GAC Asn Gln Gly Asn Ala Tyr Glu Asn His Asp Leu Gly Lys Thr Gln Asp 525 530 535	1875
TTT TCA TTT GTG CAG CTC TCT GCT CTG GGT ACT GCA ACA ACT ACA GAT Phe Ser Phe Val Gln Leu Ser Ala Leu Gly Thr Ala Thr Thr Thr Asp 540 545 550 555	1923
GTT CCA GCG GTT CCT ACA GTA GCA ACT CCT ACG CAC TAT GGG TAT CAA Val Pro Ala Val Pro Thr Val Ala Thr Pro Thr His Tyr Gly Tyr Gln 560 565 570	1971
GGT ACT TGG GGA ATG ACT TGG GTT GAT GAT ACC GCA AGC ACT CCA AAG	2019

Gly Thr Trp Gly Met Thr Trp Val Asp Asp Thr Ala Ser Thr Pro Lys			
575	580	585	
ACT AAG ACA GCG ACA TTA GCT TGG ACC AAT ACA GGC TAC CTT CCG AAT			2067
Thr Lys Thr Ala Thr Leu Ala Trp Thr Asn Thr Gly Tyr Leu Pro Asn			
590	595	600	
CCT GAG CGT CAA GGA CCT TTA GTT CCT AAT AGC CTT TGG GGA TCT TTT			2115
Pro Glu Arg Gln Gly Pro Leu Val Pro Asn Ser Leu Trp Gly Ser Phe			
605	610	615	
TCA GAC ATC CAA GCG ATT CAA GGT GTC ATA GAG AGA AGT GCT TTG ACT			2163
Ser Asp Ile Gln Ala Ile Gln Gly Val Ile Glu Arg Ser Ala Leu Thr			
620	625	630	635
CTT TGT TCA GAT CGA GGC TTC TGG GCT GCG GGA GTC GCC AAT TTC TTA			2211
Leu Cys Ser Asp Arg Gly Phe Trp Ala Ala Gly Val Ala Asn Phe Leu			
640	645	650	
GAT AAA GAT AAG AAA GGG GAA AAA CGC AAA TAC CGT CAT AAA TCT GGT			2259
Asp Lys Asp Lys Lys Gly Glu Lys Arg Lys Tyr Arg His Lys Ser Gly			
655	660	665	
GGA TAT GCT ATC GGA GGT GCA GCG CAA ACT TGT TCT GAA AAC TTA ATT			2307
Gly Tyr Ala Ile Gly Gly Ala Ala Gln Thr Cys Ser Glu Asn Leu Ile			
670	675	680	
AGC TTT GCC TTT TGC CAA CTC TTT GGT AGC GAT AAA GAT TTC TTA GTC			2355
Ser Phe Ala Phe Cys Gln Leu Phe Gly Ser Asp Lys Asp Phe Leu Val			
685	690	695	
GCT AAA AAT CAT ACT GAT ACC TAT GCA GGA GCC TTC TAT ATC CAA CAC			2403
Ala Lys Asn His Thr Asp Thr Tyr Ala Gly Ala Phe Tyr Ile Gln His			
700	705	710	715
ATT ACA GAA TGT AGT GGG TTC ATA GGT TGT CTC TTA GAT AAA CTT CCT			2451
Ile Thr Glu Cys Ser Gly Phe Ile Gly Cys Leu Leu Asp Lys Leu Pro			
720	725	730	
GGC TCT TGG AGT CAT AAA CCC CTC GTT TTA GAA GGG CAG CTC GCT TAT			2499
Gly Ser Trp Ser His Lys Pro Leu Val Leu Glu Gly Gln Leu Ala Tyr			
735	740	745	
AGC CAC GTC AGT AAT GAT CTG AAG ACA AAG TAT ACT GCG TAT CCT GAG			2547
Ser His Val Ser Asn Asp Leu Lys Thr Lys Tyr Thr Ala Tyr Pro Glu			
750	755	760	
GTG AAA GGT TCT TGG GGG AAT AAT GCT TTT AAC ATG ATG TTG GGA GCT			2595
Val Lys Gly Ser Trp Gly Asn Asn Ala Phe Asn Met Met Leu Gly Ala			
765	770	775	
TCT TCT CAT TCT TAT CCT GAA TAC CTG CAT TGT TTT GAT ACC TAT GCT			2643
Ser Ser His Ser Tyr Pro Glu Tyr Leu His Cys Phe Asp Thr Tyr Ala			
780	785	790	795
CCA TAC ATC AAA CTG AAT CTG ACC TAT ATA CGT CAG GAC AGC TTC TCG			2691
Pro Tyr Ile Lys Leu Asn Leu Thr Tyr Ile Arg Gln Asp Ser Phe Ser			
800	805	810	

GAG AAA GGT ACA GAA GGA AGA TCT TTT GAT GAC AGC AAC CTC TTC AAT Glu Lys Gly Thr Glu Gly Arg Ser Phe Asp Asp Ser Asn Leu Phe Asn 815 820 825	2739
TTA TCT TTG CCT ATA GGG GTG AAG TTT GAG AAG TTC TCT GAT TGT AAT Leu Ser Leu Pro Ile Gly Val Lys Phe Glu Lys Phe Ser Asp Cys Asn 830 835 840	2787
GAC TTT TCT TAT GAT CTG ACT TTA TCC TAT GTT CCT GAT CTT ATC CGC Asp Phe Ser Tyr Asp Leu Thr Leu Ser Tyr Val Pro Asp Leu Ile Arg 845 850 855	2835
AAT GAT CCC AAA TGC ACT ACA GCA CTT GTA ATC AGC GGA GCC TCT TGG Asn Asp Pro Lys Cys Thr Thr Ala Leu Val Ile Ser Gly Ala Ser Trp 860 865 870 875	2883
GAA ACT TAT GCC AAT AAC TTA GCA CGA CAG GCC TTG CAA GTG CGT GCA Glu Thr Tyr Ala Asn Asn Leu Ala Arg Gln Ala Leu Gln Val Arg Ala 880 885 890	2931
GGC AGT CAC TAC GCC TTC TCT CCT ATG TTT GAA GTG CTC GGC CAG TTT Gly Ser His Tyr Ala Phe Ser Pro Met Phe Glu Val Leu Gly Gln Phe 895 900 905	2979
GTC TTT GAA GTT CGT GGA TCC Val Phe Glu Val Arg Gly Ser 910	3000

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 914 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (v) FRAGMENT TYPE: internal
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Lys Ser Gln Phe Ser Trp Leu Val Leu Ser Ser Thr Leu Ala Cys	1	5	10	15
Phe Thr Ser Cys Ser Thr Val Phe Ala Ala Thr Ala Glu Asn Ile Gly				
	20	25	30	
Pro Ser Asp Ser Phe Asp Gly Ser Thr Asn Thr Gly Thr Tyr Thr Pro				
	35	40	45	
Lys Asn Thr Thr Thr Gly Ile Asp Tyr Thr Leu Thr Gly Asp Ile Thr				
	50	55	60	
Leu Gln Asn Leu Gly Asp Ser Ala Ala Leu Thr Lys Gly Cys Phe Ser				
	65	70	75	80

Asp Thr Thr Glu Ser Leu Ser Phe Ala Gly Lys Gly Tyr Ser Leu Ser
 85 90 95

 Phe Leu Asn Ile Lys Ser Ser Ala Glu Gly Ala Ala Leu Ser Val Thr
 100 105 110

 Thr Asp Lys Asn Leu Ser Leu Thr Gly Phe Ser Ser Leu Thr Phe Leu
 115 120 125

 Ala Ala Pro Ser Ser Val Ile Thr Thr Pro Ser Gly Lys Gly Ala Val
 130 135 140

 Lys Cys Gly Gly Asp Leu Thr Phe Asp Asn Asn Gly Thr Ile Leu Phe
 145 150 155 160

 Lys Gln Asp Tyr Cys Glu Glu Asn Gly Gly Ala Ile Ser Thr Lys Asn
 165 170 175

 Leu Ser Leu Lys Asn Ser Thr Gly Ser Ile Ser Phe Glu Gly Asn Lys
 180 185 190

 Ser Ser Ala Thr Gly Lys Gly Gly Ala Ile Cys Ala Thr Gly Thr
 195 200 205

 Val Asp Ile Thr Asn Asn Thr Ala Pro Thr Leu Phe Ser Asn Asn Ile
 210 215 220

 Ala Glu Ala Ala Gly Gly Ala Ile Asn Ser Thr Gly Asn Cys Thr Ile
 225 230 235 240

 Thr Gly Asn Thr Ser Leu Val Phe Ser Glu Asn Ser Val Thr Ala Thr
 245 250 255

 Ala Gly Asn Gly Gly Ala Leu Ser Gly Asp Ala Asp Val Thr Ile Ser
 260 265 270

 Gly Asn Gln Ser Val Thr Phe Ser Gly Asn Gln Ala Val Ala Asn Gly
 275 280 285

 Gly Ala Ile Tyr Ala Lys Lys Leu Thr Leu Ala Ser Gly Gly Gly
 290 295 300

 Gly Ile Ser Phe Ser Asn Asn Ile Val Gln Gly Thr Thr Ala Gly Asn
 305 310 315 320

 Gly Gly Ala Ile Ser Ile Leu Ala Ala Gly Glu Cys Ser Leu Ser Ala
 325 330 335

 Glu Ala Gly Asp Ile Thr Phe Asn Gly Asn Ala Ile Val Ala Thr Thr
 340 345 350

 Pro Gln Thr Thr Lys Arg Asn Ser Ile Asp Ile Gly Ser Thr Ala Lys
 355 360 365

 Ile Thr Asn Leu Arg Ala Ile Ser Gly His Ser Ile Phe Phe Tyr Asp
 370 375 380

Pro Ile Thr Ala Asn Thr Ala Ala Asp Ser Thr Asp Thr Leu Asn Leu
 385 390 395 400

Asn Lys Ala Asp Ala Gly Asn Ser Thr Asp Tyr Ser Gly Ser Ile Val
 405 410 415

Phe Ser Gly Glu Lys Leu Ser Glu Asp Glu Ala Lys Val Ala Asp Asn
 420 425 430

Leu Thr Ser Thr Leu Lys Gln Pro Val Thr Leu Thr Ala Gly Asn Leu
 435 440 445

Val Leu Lys Arg Gly Val Thr Leu Asp Thr Lys Gly Phe Thr Gln Thr
 450 455 460

Ala Gly Ser Ser Val Ile Met Asp Ala Gly Thr Thr Leu Lys Ala Ser
 465 470 475 480

Thr Glu Glu Val Thr Leu Thr Gly Leu Ser Ile Pro Val Asp Ser Leu
 485 490 495

Gly Glu Gly Lys Lys Val Val Ile Ala Ala Ser Ala Ala Ser Lys Asn
 500 505 510

Val Ala Leu Ser Gly Pro Ile Leu Leu Leu Asp Asn Gln Gly Asn Ala
 515 520 525

Tyr Glu Asn His Asp Leu Gly Lys Thr Gln Asp Phe Ser Phe Val Gln
 530 535 540

Leu Ser Ala Leu Gly Thr Ala Thr Thr Asp Val Pro Ala Val Pro
 545 550 555 560

Thr Val Ala Thr Pro Thr His Tyr Gly Tyr Gln Gly Thr Trp Gly Met
 565 570 575

Thr Trp Val Asp Asp Thr Ala Ser Thr Pro Lys Thr Lys Thr Ala Thr
 580 585 590

Leu Ala Trp Thr Asn Thr Gly Tyr Leu Pro Asn Pro Glu Arg Gln Gly
 595 600 605

Pro Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Ser Asp Ile Gln Ala
 610 615 620

Ile Gln Gly Val Ile Glu Arg Ser Ala Leu Thr Leu Cys Ser Asp Arg
 625 630 635 640

Gly Phe Trp Ala Ala Gly Val Ala Asn Phe Leu Asp Lys Asp Lys Lys
 645 650 655

Gly Glu Lys Arg Lys Tyr Arg His Lys Ser Gly Gly Tyr Ala Ile Gly
 660 665 670

Gly Ala Ala Gln Thr Cys Ser Glu Asn Leu Ile Ser Phe Ala Phe Cys
 675 680 685

Gln Leu Phe Gly Ser Asp Lys Asp Phe Leu Val Ala Lys Asn His Thr
 690 695 700

Asp Thr Tyr Ala Gly Ala Phe Tyr Ile Gln His Ile Thr Glu Cys Ser
 705 710 715 720

Gly Phe Ile Gly Cys Leu Leu Asp Lys Leu Pro Gly Ser Trp Ser His
 725 730 735

Lys Pro Leu Val Leu Glu Gly Gln Leu Ala Tyr Ser His Val Ser Asn
 740 745 750

Asp Leu Lys Thr Lys Tyr Thr Ala Tyr Pro Glu Val Lys Gly Ser Trp
 755 760 765

Gly Asn Asn Ala Phe Asn Met Met Leu Gly Ala Ser Ser His Ser Tyr
 770 775 780

Pro Glu Tyr Leu His Cys Phe Asp Thr Tyr Ala Pro Tyr Ile Lys Leu
 785 790 795 800

Asn Leu Thr Tyr Ile Arg Gln Asp Ser Phe Ser Glu Lys Gly Thr Glu
 805 810 815

Gly Arg Ser Phe Asp Asp Ser Asn Leu Phe Asn Leu Ser Leu Pro Ile
 820 825 830

Gly Val Lys Phe Glu Lys Phe Ser Asp Cys Asn Asp Phe Ser Tyr Asp
 835 840 845

Leu Thr Leu Ser Tyr Val Pro Asp Leu Ile Arg Asn Asp Pro Lys Cys
 850 855 860

Thr Thr Ala Leu Val Ile Ser Gly Ala Ser Trp Glu Thr Tyr Ala Asn
 865 870 875 880

Asn Leu Ala Arg Gln Ala Leu Gln Val Arg Ala Gly Ser His Tyr Ala
 885 890 895

Phe Ser Pro Met Phe Glu Val Leu Gly Gln Phe Val Phe Glu Val Arg
 900 905 910

Gly Ser

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...1200
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAT CCT AAA AAT AAA GAG TAC ACA GGG ACC ATA CTC TTT TCT GGA GAA Asp Pro Lys Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu 1 5 10 15	48
AAG AGT CTA GCA AAC GAT CCT AGG GAT TTT AAA TCT ACA ATC CCT CAG Lys Ser Leu Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln 20 25 30	96
AAC GTC AAC CTG TCT GCA GGA TAC TTA GTT ATT AAA GAG GGG GCC GAA Asn Val Asn Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu 35 40 45	144
GTC ACA GTT TCA AAA TTC ACG CAG TCT CCA GGA TCG CAT TTA GTT TTA Val Thr Val Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu 50 55 60	192
GAT TTA GGA ACC AAA CTG ATA GCC TCT AAG GAA GAC ATT GCC ATC ACA Asp Leu Gly Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr 65 70 75 80	240
GGC CTC GCG ATA GAT ATA GAT AGC TTA AGC TCA TCC TCA ACA GCA GCT Gly Leu Ala Ile Asp Ile Asp Ser Leu Ser Ser Ser Thr Ala Ala 85 90 95	288
GTT ATT AAA GCA AAC ACC GCA AAT AAA CAG ATA TCC GTG ACG GAC TCT Val Ile Lys Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser 100 105 110	336
ATA GAA CTT ATC TCG CCT ACT GGC AAT GCC TAT GAA GAT CTC AGA ATG Ile Glu Leu Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met 115 120 125	384
AGA AAT TCA CAG ACG TTC CCT CTG CTC TCT TTA GAG CCT GGA GCC GGG Arg Asn Ser Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly 130 135 140	432
GGT AGT GTG ACT GTA ACT GCT GGA GAT TTC CTA CCG GTA AGT CCC CAT Gly Ser Val Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His 145 150 155 160	480
TAT GGT TTT CAA GGC AAT TGG AAA TTA GCT TGG ACA GGA ACT GGA AAC Tyr Gly Phe Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn 165 170 175	528
AAA GTT GGA GAA TTC TTC TGG GAT AAA ATA AAT TAT AAG CCT AGA CCT Lys Val Gly Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro 180 185 190	576
GAA AAA GAA GGA AAT TTA GTT CCT AAT ATC TTG TGG GGG AAT GCT GTA Glu Lys Glu Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val 195 200 205	624
AAT GTC AGA TCC TTA ATG CAG GTT CAA GAG ACC CAT GCA TCG AGC TTA Asn Val Arg Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu 210 215 220	672

CAG ACA GAT CGA GGG CTG TGG ATC GAT GGA ATT GGG AAT TTC TTC CAT		720
Gln Thr Asp Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Phe Phe His		
225	230	235
240		
GTA TCT GCC TCC GAA GAC AAT ATA AGG TAC CGT CAT AAC AGC GGT GGA		768
Val Ser Ala Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly		
245	250	255
TAT GTT CTA TCT GTA AAT AAT GAG ATC ACA CCT AAG CAC TAT ACT TCG		816
Tyr Val Leu Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser		
260	265	270
ATG GCA TTT TCC CAA CTC TTT AGT AGA GAC AAA GAC TAT GCG GTT TCC		864
Met Ala Phe Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser		
275	280	285
AAC AAC GAA TAC AGA ATG TAT TTA GGA TCG TAT CTC TAT CAA TAT ACA		912
Asn Asn Glu Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr		
290	295	300
ACC TCC CTA GGG AAT ATT TTC CGT TAT GCT TCG CGT AAC CCT AAT GTA		960
Thr Ser Leu Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val		
305	310	315
320		
AAC GTC GGG ATT CTC TCA AGA AGG TTT CTT CAA AAT CCT CTT ATG ATT		1008
Asn Val Gly Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile		
325	330	335
TTT CAT TTT TTG TGT GCT TAT GGT CAT GCC ACC AAT GAT ATG AAA ACA		1056
Phe His Phe Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr		
340	345	350
GAC TAC GCA AAT TTC CCT ATG GTG AAA AAC AGC TGG AGA AAC AAT TGT		1104
Asp Tyr Ala Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys		
355	360	365
TGG GCT ATA AAA TGC GGA GGG AGC ATG CCT CTA TTG GTA TTT GAA AAC		1152
Trp Ala Ile Lys Cys Gly Ser Met Pro Leu Leu Val Phe Glu Asn		
370	375	380
GGA AAA CTT TTC CAA GGT GCC ATC CCA TTT ATG AAA CTA CAA TTA GTT		1200
Gly Lys Leu Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val		
385	390	395
390		400

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Asp Pro Lys Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu
 1 5 10 15

Lys Ser Leu Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln
 20 25 30

Asn Val Asn Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu
 35 40 45

Val Thr Val Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu
 50 55 60

Asp Leu Gly Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr
 65 70 75 80

Gly Leu Ala Ile Asp Ile Asp Ser Leu Ser Ser Ser Ser Thr Ala Ala
 85 90 95

Val Ile Lys Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser
 100 105 110

Ile Glu Leu Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met
 115 120 125

Arg Asn Ser Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly
 130 135 140

Gly Ser Val Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His
 145 150 155 160

Tyr Gly Phe Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn
 165 170 175

Lys Val Gly Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro
 180 185 190

Glu Lys Glu Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val
 195 200 205

Asn Val Arg Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu
 210 215 220

Gln Thr Asp Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Phe Phe His
 225 230 235 240

Val Ser Ala Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly
 245 250 255

Tyr Val Leu Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser
 260 265 270

Met Ala Phe Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser
 275 280 285

Asn Asn Glu Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr
 290 295 300

Thr Ser Leu Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val
 305 310 315 320
 Asn Val Gly Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile
 325 330 335
 Phe His Phe Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr
 340 345 350
 Asp Tyr Ala Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys
 355 360 365
 Trp Ala Ile Lys Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn
 370 375 380
 Gly Lys Leu Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val
 385 390 395 400

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1830 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...1830
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAT CTC ACA TTA GGG AGT CGT GAC AGT TAT AAT GGT GAT ACA AGC ACC	48
Asp Leu Thr Leu Gly Ser Arg Asp Ser Tyr Asn Gly Asp Thr Ser Thr	
1 5 10 15	
ACA GAA TTT ACT CCT AAA GCG GCA ACT TCT GAT GCT AGT GGC ACG ACC	96
Thr Glu Phe Thr Pro Lys Ala Ala Thr Ser Asp Ala Ser Gly Thr Thr	
20 25 30	
TAT ATT CTC GAT GGG GAT GTC TCG ATA AGC CAA GCA GGG AAA CAA ACG	144
Tyr Ile Leu Asp Gly Asp Val Ser Ile Ser Gln Ala Gly Lys Gln Thr	
35 40 45	
AGC TTA ACC ACA AGT TGT TTT TCT AAC ACT GCA GGA AAT CTT ACC TTC	192
Ser Leu Thr Thr Ser Cys Phe Ser Asn Thr Ala Gly Asn Leu Thr Phe	
50 55 60	
TTA GGG AAC GGA TTT TCT CTT CAT TTT GAC AAT ATT ATT TCG TCT ACT	240
Leu Gly Asn Gly Phe Ser Leu His Phe Asp Asn Ile Ile Ser Ser Thr	
65 70 75 80	
GTT GCA GGT GTT GTT AGC AAT ACA GCA GCT TCT GGG ATT ACG AAA	288
Val Ala Gly Val Val Val Ser Asn Thr Ala Ala Ser Gly Ile Thr Lys	

85	90	95	
TTC TCA GGA TTT TCA ACT CTT CGG ATG CTT GCA GCT CCT AGG ACC ACA Phe Ser Gly Phe Ser Thr Leu Arg Met Leu Ala Ala Pro Arg Thr Thr 100	105	110	336
GGT AAA GGA GCC ATT AAA ATT ACC GAT GGT CTG GTG TTT GAG AGT ATA Gly Lys Gly Ala Ile Lys Ile Thr Asp Gly Leu Val Phe Glu Ser Ile 115	120	125	384
GGG AAT CTT GAT CCG ATT ACT GTA ACA GGA TCG ACA TCT GTT GCT GAT Gly Asn Leu Asp Pro Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp 130	135	140	432
GCT CTC AAT ATT AAT AGC CCT GAT ACT GGA GAT AAC AAA GAG TAT ACG Ala Leu Asn Ile Asn Ser Pro Asp Thr Gly Asp Asn Lys Glu Tyr Thr 145	150	155	480
GGA ACC ATA GTC TTT TCT GGA GAG AAG CTC ACG GAG GCA GAA GCT AAA Gly Thr Ile Val Phe Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys 165	170	175	528
GAT GAG AAG AAC CGC ACT TCT AAA TTA CTT CAA AAT GTT GCT TTT AAA Asp Glu Lys Asn Arg Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys 180	185	190	576
AAT GGG ACT GTA GTT TTA AAA GGT GAT GTC GTT TTA AGT GCG AAC GGT Asn Gly Thr Val Val Leu Lys Gly Asp Val Val Leu Ser Ala Asn Gly 195	200	205	624
TTC TCT CAG GAT GCA AAC TCT AAG TTG ATT ATG GAT TTA GGG ACG TCG Phe Ser Gln Asp Ala Asn Ser Lys Leu Ile Met Asp Leu Gly Thr Ser 210	215	220	672
TTG GTT GCA AAC ACC GAA AGT ATC GAG TTA ACG AAT TTG GAA ATT AAT Leu Val Ala Asn Thr Glu Ser Ile Glu Leu Thr Asn Leu Glu Ile Asn 225	230	235	720
ATA GAC TCT CTC AGG AAC GGG AAA AAG ATA AAA CTC AGT GCT GCC ACA Ile Asp Ser Leu Arg Asn Gly Lys Lys Ile Lys Leu Ser Ala Ala Thr 245	250	255	768
GCT CAG AAA GAT ATT CGT ATA GAT CGT CCT GTT GTA CTG GCA ATT AGC Ala Gln Lys Asp Ile Arg Ile Asp Arg Pro Val Val Leu Ala Ile Ser 260	265	270	816
GAT GAG AGT TTT TAT CAA AAT GGC TTT TTG AAT GAG GAC CAT TCC TAT Asp Glu Ser Phe Tyr Gln Asn Gly Phe Leu Asn Glu Asp His Ser Tyr 275	280	285	864
GAT GGG ATT CTT GAG TTA GAT GCT GGG AAA GAC ATC GTG ATT TCT GCA Asp Gly Ile Leu Glu Leu Asp Ala Gly Lys Asp Ile Val Ile Ser Ala 290	295	300	912
GAT TCT CGC AGT ATA GAT GCT GTA CAA TCT CCG TAT GGC TAT CAG GGA Asp Ser Arg Ser Ile Asp Ala Val Gln Ser Pro Tyr Gly Tyr Gln Gly 305	310	315	960

AAG TGG ACG ATC AAT TGG TCT ACT GAT GAT AAG AAA GCT ACG GTT TCT		1008
Lys Trp Thr Ile Asn Trp Ser Thr Asp Asp Lys Lys Ala Thr Val Ser		
325 330 335		
TGG GCG AAG CAG AGT TTT AAT CCC ACT GCT GAG CAG GAG GCT CCG TTA		1056
Trp Ala Lys Gln Ser Phe Asn Pro Thr Ala Glu Gln Glu Ala Pro Leu		
340 345 350		
GTT CCT AAT CTT CTT TGG GGT TCT TTT ATA GAT GTT CGT TCC TTC CAG		1104
Val Pro Asn Leu Leu Trp Gly Ser Phe Ile Asp Val Arg Ser Phe Gln		
355 360 365		
AAT TTT ATA GAG CTA GGT ACT GAA GGT GCT CCT TAC GAA AAG AGA TTT		1152
Asn Phe Ile Glu Leu Gly Thr Glu Gly Ala Pro Tyr Glu Lys Arg Phe		
370 375 380		
TGG GTT GCA GGC ATT TCC AAT GTT TTG CAT AGG AGC GGT CGT GAA AAT		1200
Trp Val Ala Gly Ile Ser Asn Val Leu His Arg Ser Gly Arg Glu Asn		
385 390 395 400		
CAA AGG AAA TTC CGT CAT GTG AGT GGA GGT GCT GTA GTA GGT GCT AGC		1248
Gln Arg Lys Phe Arg His Val Ser Gly Gly Ala Val Val Gly Ala Ser		
405 410 415		
ACG AGG ATG CCG GGT GGT GAT ACC TTG TCT CTG GGT TTT GCT CAG CTC		1296
Thr Arg Met Pro Gly Gly Asp Thr Leu Ser Leu Gly Phe Ala Gln Leu		
420 425 430		
TTT GCG CGT GAC AAA GAC TAC TTT ATG AAT ACC AAT TTC GCA AAG ACC		1344
Phe Ala Arg Asp Lys Asp Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr		
435 440 445		
TAC GCA GGA TCT TTA CGT TTG CAG CAC GAT GCT TCC CTA TAC TCT GTG		1392
Tyr Ala Gly Ser Leu Arg Leu Gln His Asp Ala Ser Leu Tyr Ser Val		
450 455 460		
GTG AGT ATC CTT TTA GGA GAG GGA GGA CTC CGC GAG ATC CTG TTG CCT		1440
Val Ser Ile Leu Leu Gly Glu Gly Gly Leu Arg Glu Ile Leu Leu Pro		
465 470 475 480		
TAT GTT TCC AAT ACT CTG CCG TGC TCT TTC TAT GGG CAG CTT AGC TAC		1488
Tyr Val Ser Asn Thr Leu Pro Cys Ser Phe Tyr Gly Gln Leu Ser Tyr		
485 490 495		
GGC CAT ACG GAT CAT CGC ATG AAG ACC GAG TCT CTA CCC CCC CCC CCC		1536
Gly His Thr Asp His Arg Met Lys Thr Glu Ser Leu Pro Pro Pro Pro		
500 505 510		
CCG ACG CTC TCG ACG GAT CAT ACT TCT TGG GGA GGA TAT GTC TGG GCT		1584
Pro Thr Leu Ser Thr Asp His Thr Ser Trp Gly Gly Tyr Val Trp Ala		
515 520 525		
GGA GAG CTG GGA ACT CGA GTT GCT GTT GAA AAT ACC AGC GGC AGA GGA		1632
Gly Glu Leu Gly Thr Arg Val Ala Val Glu Asn Thr Ser Gly Arg Gly		
530 535 540		
TTT TTC CGA GAG TAC ACT CCA TTT GTA AAA GTC CAA GCT GTT TAC TCG		1680
Phe Phe Arg Glu Tyr Thr Pro Phe Val Lys Val Gln Ala Val Tyr Ser		

545	550	555	560	
CGC CAA GAT AGC TTT GTT GAA CTA GGA GCT ATC AGT CGT GAT TTT AGT Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser 565 570 575				1728
GAT TCG CAT CTT TAT AAC CTT GCG ATT CCT CTT GGA ATC AAG TTA GAG Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu 580 585 590				1776
AAA CGG TTT GCA GAG CAA TAT TAT CAT GTT GTT GCG ATG TAT TCT CCA Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro 595 600 605				1824
GAT GTT Asp Val 610				1830

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 610 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Asp Leu Thr Leu Gly Ser Arg Asp Ser Tyr Asn Gly Asp Thr Ser Thr 1 5 10 15			
Thr Glu Phe Thr Pro Lys Ala Ala Thr Ser Asp Ala Ser Gly Thr Thr 20 25 30			
Tyr Ile Leu Asp Gly Asp Val Ser Ile Ser Gln Ala Gly Lys Gln Thr 35 40 45			
Ser Leu Thr Thr Ser Cys Phe Ser Asn Thr Ala Gly Asn Leu Thr Phe 50 55 60			
Leu Gly Asn Gly Phe Ser Leu His Phe Asp Asn Ile Ile Ser Ser Thr 65 70 75 80			
Val Ala Gly Val Val Val Ser Asn Thr Ala Ala Ser Gly Ile Thr Lys 85 90 95			
Phe Ser Gly Phe Ser Thr Leu Arg Met Leu Ala Ala Pro Arg Thr Thr 100 105 110			
Gly Lys Gly Ala Ile Lys Ile Thr Asp Gly Leu Val Phe Glu Ser Ile 115 120 125			
Gly Asn Leu Asp Pro Ile Thr Val Thr Gly Ser Thr Ser Val Ala Asp			

130	135	140
Ala Leu Asn Ile Asn Ser Pro Asp Thr Gly Asp Asn Lys Glu Tyr Thr		
145	150	155
Gly Thr Ile Val Phe Ser Gly Glu Lys Leu Thr Glu Ala Glu Ala Lys		
165	170	175
Asp Glu Lys Asn Arg Thr Ser Lys Leu Leu Gln Asn Val Ala Phe Lys		
180	185	190
Asn Gly Thr Val Val Leu Lys Gly Asp Val Val Leu Ser Ala Asn Gly		
195	200	205
Phe Ser Gln Asp Ala Asn Ser Lys Leu Ile Met Asp Leu Gly Thr Ser		
210	215	220
Leu Val Ala Asn Thr Glu Ser Ile Glu Leu Thr Asn Leu Glu Ile Asn		
225	230	235
Ile Asp Ser Leu Arg Asn Gly Lys Lys Ile Lys Leu Ser Ala Ala Thr		
245	250	255
Ala Gln Lys Asp Ile Arg Ile Asp Arg Pro Val Val Leu Ala Ile Ser		
260	265	270
Asp Glu Ser Phe Tyr Gln Asn Gly Phe Leu Asn Glu Asp His Ser Tyr		
275	280	285
Asp Gly Ile Leu Glu Leu Asp Ala Gly Lys Asp Ile Val Ile Ser Ala		
290	295	300
Asp Ser Arg Ser Ile Asp Ala Val Gln Ser Pro Tyr Gly Tyr Gln Gly		
305	310	315
Lys Trp Thr Ile Asn Trp Ser Thr Asp Asp Lys Lys Ala Thr Val Ser		
325	330	335
Trp Ala Lys Gln Ser Phe Asn Pro Thr Ala Glu Gln Glu Ala Pro Leu		
340	345	350
Val Pro Asn Leu Leu Trp Gly Ser Phe Ile Asp Val Arg Ser Phe Gln		
355	360	365
Asn Phe Ile Glu Leu Gly Thr Glu Gly Ala Pro Tyr Glu Lys Arg Phe		
370	375	380
Trp Val Ala Gly Ile Ser Asn Val Leu His Arg Ser Gly Arg Glu Asn		
385	390	395
400		
Gln Arg Lys Phe Arg His Val Ser Gly Gly Ala Val Val Gly Ala Ser		
405	410	415
Thr Arg Met Pro Gly Gly Asp Thr Leu Ser Leu Gly Phe Ala Gln Leu		
420	425	430
Phe Ala Arg Asp Lys Asp Tyr Phe Met Asn Thr Asn Phe Ala Lys Thr		
435	440	445

Tyr Ala Gly Ser Leu Arg Leu Gln His Asp Ala Ser Leu Tyr Ser Val
450 455 460

Val Ser Ile Leu Leu Gly Glu Gly Gly Leu Arg Glu Ile Leu Leu Pro
465 470 475 480

Tyr Val Ser Asn Thr Leu Pro Cys Ser Phe Tyr Gly Gln Leu Ser Tyr
485 490 495

Gly His Thr Asp His Arg Met Lys Thr Glu Ser Leu Pro Pro Pro Pro
500 505 510

Pro Thr Leu Ser Thr Asp His Thr Ser Trp Gly Gly Tyr Val Trp Ala
515 520 525

Gly Glu Leu Gly Thr Arg Val Ala Val Glu Asn Thr Ser Gly Arg Gly
530 535 540

Phe Phe Arg Glu Tyr Thr Pro Phe Val Lys Val Gln Ala Val Tyr Ser
545 550 555 560

Arg Gln Asp Ser Phe Val Glu Leu Gly Ala Ile Ser Arg Asp Phe Ser
565 570 575

Asp Ser His Leu Tyr Asn Leu Ala Ile Pro Leu Gly Ile Lys Leu Glu
580 585 590

Lys Arg Phe Ala Glu Gln Tyr Tyr His Val Val Ala Met Tyr Ser Pro
595 600 605

Asp Val
610